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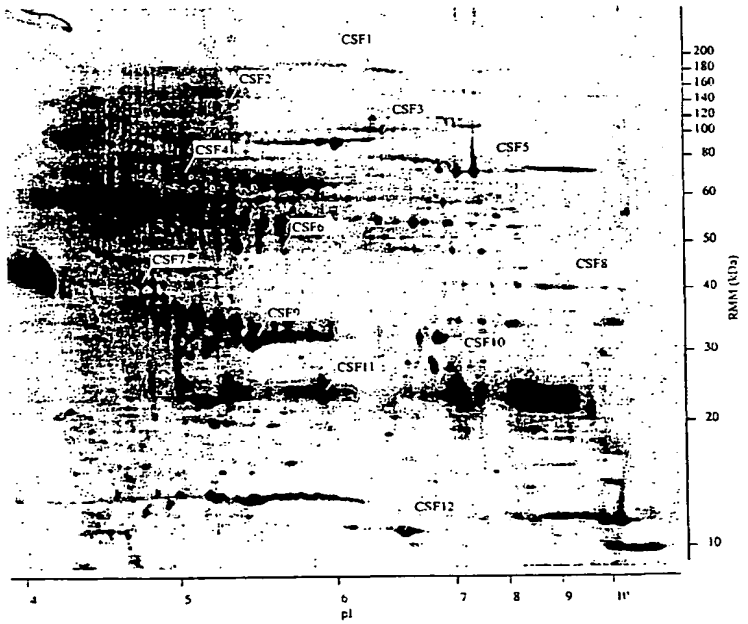
(54) Title: DIAGNOSIS AND TREATMENT OF BIPOLAR AFFECTIVE DISORDER



(57) Abstract: The present invention provides methods and compositions for screening, diagnosis and prognosis of BAD, for monitoring the effectiveness of BAD treatment, and for drug development. BAD-Associated Features (DFs), detectable by two-dimensional electrophoresis of cerebrospinal fluid, serum or plasma are described. The invention further provides BAD-Associated Protein Isoforms (DPIs) detectable in cerebrospinal fluid, serum or plasma, preparations comprising isolated DPIs, antibodies immunospecific for DPIs, and kits comprising the aforesaid.

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DIAGNOSIS AND TREATMENT OF BIPOLAR AFFECTIVE DISORDER

1. INTRODUCTION

The present invention relates to the identification of proteins and protein isoforms that are associated with Bipolar Affective Disorder (BAD) and Unipolar depression and its onset and development, and of genes encoding the same, and to their use for e.g., clinical screening, diagnosis, prognosis, therapy and prophylaxis, as well as for drug screening and drug development in the treatment of a neuropsychiatric disorder, including, by way of example and not of limitation, attention deficit disorder, a schizoaffective disorder, a bipolar affective disorder or unipolar affective disorder. For convenience, such disorders are referred to herein as BAD unless the context suggests otherwise.

2. BACKGROUND OF THE INVENTION

In the majority of psychiatric disorders, little is known about a link between changes at a cellular or molecular level and nervous system structure and function. The paucity of detectable neurologic defects distinguishes neuropsychiatric disorders such as attention deficit disorder, schizoaffective disorder, bipolar affective disorder or unipolar affective disorder from neurological disorders where manifestations of anatomical and biochemical changes have been identified. Consequently the identification and characterization of cellular or molecular causative defects and neuropathologies is desirable for improved treatment of neuropsychiatric disorders. BAD (manic-depressive illnesses), also known as bipolar mood disorder (BP) or manic-depressive illness is one of the most common, severe and often life threatening neuropsychiatric disorders. Suicide is the cause of death in 10% to 20% of individuals with either bipolar or recurrent disorders, and the risks of suicide in bipolar disorder may be higher than those in unipolar depression (reviewed by Simpson and Jamison, J Clin Psychiatry 1999, 60, 53-56). BAD is characterized by episodes of elevated mood(mania) and depression (Goodwin et al. 1990, Manic Depressive Illness, Oxford University Press, New York). BP-1 (severe bipolar affective (mood) disorder) affect2-3 million people in the US and combined with SAD-M (schizoaffective manic

type)represent the two most severe and clinically distinctive forms of BAD. BP-1 and SAD-M are always associated with at least one full episode of mania and may include episodes of depression (lowered mood and disturbances in rhythmic behaviors like sleeping, eating, and sexual activity). Since BP-1 and SAD-M follow similar clinical courses and segregate together in family studies (Rosenthal et al. 1980, Arch. General Psychiat. 37, 804-810; Levinson and Levitt, 1987, Am J Psychiat. 144, 415-426;Goddwin et al. 1990, Manic Depressive Illness, Oxford University Press, New York)they are frequently difficult to distinguish from one another. BP-1 often also co-segregates in families with unipolar major depressive disorder (MDD), which has a broadly defined phenotype (Freimer and Reus, 1992, in The Molecular and GeneticBasis of Neurological Disease, Rosenberget al. Eds., Butterworths, New York, pp.951-965; McInnes and Freimer, 1995, Curr. Opin. Genet. Develop., 5, 376-381). The identification of proteins and protein isoforms that are associated with the onset and progression of various forms of depression would be desirable for the effective diagnosis, prognosis and treatment of afflicted individuals.

Major mood disorders are also associated with many other deleterious health related effects and the costs with disability and premature death represent an economic burden of $43 billion annually in the United States alone. Rates of depression co-occurring with other medical conditions are as follows: myocardial infarction:20-40%, Parkinson's disease: 40%, Alzheimer's disease: 30-35%, stroke: 25-50%,cancer: 3-50%, HIV/AIDS: 10-20 %, rheumatoid arthritis: 12 %, diabetes mellitus:14-18%, chronic pain: 30%, disabling tinnitus: 60%, end-stage renal disease: 5-22%and spinal cord injury: 37% (Goldman et al. J Gen Intern Med 1999, 14, 569-580;Wyatt and Henter 1995, Soc Psychiatry Psychiatr Epidemiolm 30, 213-219). Despite the devastating impact of these disorders on the lives of millions, there is still uncertainty about the differential diagnosis of depression in the presence of these disorders (Goldman et al. 1999, J Gen Med 14, 569-80; Schatzberg 1998, J ClinPsychiatry, 59, suppl 6:5-12; Goodwin and Jamison, 1990 Manic-depressive illness, New York, Oxford University Press).

Major depression is a syndromal diagnosis: on the basis of the patient's medical history and physical examination, it may be appropriate to consider other psychiatric disorders and general medical conditions (Goldman et al. J Gen Intern Med 1999, 14, 569-580) but very limited knowledge exists concerning their etiology and pathophysiology (Ikonomov et al. 1999, Am J Psychiatry, 156, 1506-

1514).Genetic segregation analyses and twin studies suggest genetic element for BAD (Bertelsonet al. 1977, Br. J. Psychiat. 130, 330-351; Freimer and Reus, 1992, in The Molecular and Genetic Basis of Neurological Disease, Rosenberg et al. Eds., Butterworths, New York, pp. 951-965; Pauls et al. 1992, Arch. Gen. Psychiat. 49,703-708). Although several localizations for BAD genes have been proposed on chromosome 18p and 21q and candidate regions for possible gene locations are now well defined, no genes associated with the disease have been identified yet (Berrettiniet al. 1994, Proc. Natl. Acad. Sci., USA 91, 5918-5921; Murray et al. 1994, Science265, 2049-2054; Pauls et al. 1995, Am. J. Hum. Genet. 57, 636-643; Maier et al. 1995,Psych. Res. 59, 7-15).

Major depression is a frequent diagnosis in patients evaluated for both cognitive and affective disorders and many depressed patients, in fact, are clinically characterized by cognitive impairments (Emery and Oxman, 1992, Am J Psychiatry,149, 305-317).

Current therapeutic can be categorized into the following major classes of agents: mood stabilizers: lithium, divalproex, carbamazepine, lamotrigine; antidepressants: tricyclic antidepressants (eg. Desipramine, chlorimipramine, nortriptyline), selective serotonin re uptake inhibitors (SSRIs including fluoxetine(Prozac), sertraltrine (Zoloft), paroxitene (Paxil), fluvoxamine (Luvox), andcitalopram (Celexa)), MAOIs, bupropion (Wellbutrin), venlafaxine (Effexor), andmirtazapine (Remeron); and atypical antipsychotic agents: Clozapine, Olanzapine, Risperidone. However, the cellular and molecular basis for the efficacy of currently used mood-stabilizing and mortality-lowering agents remains to be fully elucidated(Manji et al. 1999, J Clin Psychiatry, 60, 27-39). A significant number of patients respond poorly to existing therapies such as lithium, while many others are helped but continue to suffer significant morbidity (Chou 1991, J Clin Psychopharmacol 11,3-21). The recognition of the significant morbidity and mortality of the severe mood disorders, as well as the growing appreciation that a significant percentage of patients respond poorly to existing treatments, has made the task of developing new therapeutic agents that work quickly, potently, specifically, and with fewer side effects one of major public health importance (Bebchuk et al. Arch Gen Psychiatry 2000 57,95-7). Hence it would be highly desirable to measure a substance or substances in samples of cerebrospinal fluid (CSF), blood or urine that would lead to a positive diagnosis of BAD or that would help to exclude or include BAD from a

differential diagnosis. Since the CSF bathes the brain, changes in its protein composition may most accurately reveal alterations in brain protein expression pattern causatively or diagnostically linked to the disease.

Although genetics and genotyping may help to define the heritable risk for BAD, the utility of genetic based procedures for diagnosis, prognosis and treatment of BAD may be considerably less. Furthermore, no CNS tissue necessary for any gene expression analysis can be obtained for a living patient under normal circumstances. Proteomic approaches appear most suitable for a molecular dissection of such disease phenotype in the central nervous system (CNS). The entire CNS is largely inaccessible to meaningful mRNA expression-based analyses of primary human material, since post mortem delays in primary human brain tissue affects mRNAs more readily than proteins (Edgar, P.F., Schonberger, S.J., Dean, B., Faull, R.L.M., Kydd, R., Cooper, G.J.S. Molecular Psychiatry 1999, 4, 173-17.). Given that the CSF bathes the brain, changes in its protein composition may reveal alterations in CNS protein expression pattern causatively or diagnostically linked to the disease. Reasonable amounts of disease associated proteins (DAPs) are secreted or released into body fluids by diseased tissue in the living patient at the onset and/or during progression of the disease. In many cases these alterations will be independent of the genetic makeup of the individual and rather directly related to a set of molecular and cellular alterations contribution to the pathogenic phenotype.

Therefore, a need exists to identify sensitive and specific biomarkers for the diagnosis, to assess severity and predict the outcome of BAD in living subjects. Additionally, there is a clear need for new therapeutic agents for BAD that work quickly, potently, specifically, and with fewer side effects.

3. SUMMARY OF THE INVENTION

The present invention provides methods and compositions for clinical screening, diagnosis, prognosis, therapy and prophylaxis of BAD, for monitoring the effectiveness of BAD treatment, for selecting participants in clinical trials, for identifying patients most likely to respond to a particular therapeutic treatment and for screening and development of drugs for treatment of BAD.A first aspect of the invention provides methods for diagnosis of BAD that comprise analyzing a sample of CSF by two-dimensional electrophoresis to detect the presence or level of at least one Depression-Associated Feature (DF), e.g., one or more of the DFs disclosed

herein, or any combination thereof. These methods are also suitable for clinical screening, prognosis, monitoring the results of therapy, for identifying patients most likely to respond to a particular therapeutic treatment, drug screening and development, and identification of new targets for drug treatment.

A second aspect of the invention provides methods for diagnosis of BAD that comprise detecting in a sample of CSF the presence or level of at least one Depression-Associated Protein Isoform (DPI), e.g., one or more of the DPIs disclosed herein or any combination thereof. These methods are also suitable for clinical screening, prognosis, monitoring the results of therapy, identifying patients most likely to respond to a particular therapeutic treatment drug screening and development, and identification of new targets for drug treatment.

A third aspect of the invention provides antibodies, e.g., monoclonal and polyclonal capable of immunospecific binding to a DPI, e.g., a DPI disclosed herein.

A fourth aspect of the invention provides a preparation comprising an isolated DPI, i.e., a DPI free from proteins or protein isoforms having a significantly different isoelectric point or a significantly different apparent molecular weight from the DPI.

A fifth aspect of the invention provides methods of treating BAD, comprising administering to a subject a therapeutically effective amount of an agent that modulates (e.g., upregulates or downregulates) the expression or activity (e.g., enzymatic or binding activity), or both, of a DPI in subjects having BAD, in order to prevent or delay the onset or development of BAD, to prevent or delay the progression of BAD, or to ameliorate the symptoms of BAD.

A sixth aspect of the invention provides methods of screening for agents that modulate (e.g., upregulate or downregulate) a characteristic of, e.g., the expression or the enzymatic or binding activity, of a DPI, a DPI analog, or a DPI-related polypeptide.

3.1. DEFINITIONS

The term "DPI analog" as used herein refers to a polypeptide that possesses similar or identical function(s) as a DPI but need not necessarily comprise an amino acid sequence that is similar or identical to the amino acid sequence of the DPI, or possess a structure that is similar or identical to that of the DPI. As used herein, an amino acid sequence of a polypeptide is "similar" to that of a DPI if it satisfies at leastone of the following criteria: (a) the polypeptide has an amino acid sequence that

is at least 30% (more preferably, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least85%, at least 90%, at least 95% or at least 99%) identical to the amino acid sequence of the DPI; (b) the polypeptide is encoded by a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence encoding at least 5 amino acid residues (more preferably, at least 10 amino acid residues, at least 15 amino acid residues, at least 20 amino acid residues, at least 25 amino acid residues, at least 40amino acid residues, at least 50 amino acid residues, at least 60 amino residues, at least 70 amino acid residues, at least 80 amino acid residues, at least 90 amino acid residues, at least 100 amino acid residues, at least 125 amino acid residues, or at least150 amino acid residues) of the DPI; or (c) the polypeptide is encoded by a nucleotide sequence that is at least 30% (more preferably, at least 35%, at least 40%, at least45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%,at least 80%, at least 85%, at least 90%, at least 95% or at least 99%) identical to the nucleotide sequence encoding the DPI. As used herein, a polypeptide with "similar structure" to that of a DPI refers to a polypeptide that has a similar secondary, tertiary or quarternary structure as that of the DPI. The structure of a polypeptide can determined by methods known to those skilled in the art, including but not limited to, X-ray crystallography, nuclear magnetic resonance, and crystallographic electron microscopy.

The term "DPI fusion protein" as used herein refers to a polypeptide that comprises (i) an amino acid sequence of a DPI, a DPI fragment, a DPI-related polypeptide or a fragment of a DPI-related polypeptide and (ii) an amino acid sequence of a heterologous polypeptide (i.e., a non-DPI, non-DPI fragment or non-DPI-related polypeptide).

The term "DPI homolog" as used herein refers to a polypeptide that comprises an amino acid sequence similar to that of a DPI but does not necessarily possess a similar or identical function as the DPI.

The term "DPI ortholog" as used herein refers to a non-human polypeptide that(i) comprises an amino acid sequence similar to that of a DPI and (ii) possesses a similar or identical function to that of the DPI.

The term "DPI-related polypeptide" as used herein refers to a DPI homolog, a DPI analog, an isoform of DPI, a DPI ortholog, or any combination thereof.

The term "derivative" as used herein refers to a polypeptide that comprises an amino acid sequence of a second polypeptide which has been altered by the introduction of amino acid residue substitutions, deletions or additions. The derivative polypeptide possess a similar or identical function as the second polypeptide.

The term "fragment" as used herein refers to a peptide or polypeptide comprising an amino acid sequence of at least 5 amino acid residues (preferably, at least 10 amino acid residues, at least 15 amino acid residues, at least 20 amino acid residues, at least 25 amino acid residues, at least 40 amino acid residues, at least 50amino acid residues, at least 60 amino residues, at least 70 amino acid residues, at least 80 amino acid residues, at least 90 amino acid residues, at least 100 amino acid residues, at least 125 amino acid residues, at least 150 amino acid residues, at least175 amino acid residues, at least 200 amino acid residues, or at least 250 amino acid residues) of the amino acid sequence of a second polypeptide. The fragment of a DPI may or may not possess a functional activity of the a second polypeptide.

The term "fold change" includes "fold increase" and "fold decrease" and refers to the relative increase or decrease in abundance of an DF or the relative increase or decrease in expression or activity of a polypeptide (e.g. a DPI) in a first sample or sample set compared to a second sample (or sample set). A DF or polypeptide fold change may be measured by any technique known to those of skill in the art, albeit the observed increase or decrease will vary depending upon the technique used. Preferably, fold change is determined herein as described in the Examples infra.

The term "isoform" as used herein refers to variants of a polypeptide that are encoded by the same gene, but that differ in their pI or MW, or both. Such isoforms can differ in their amino acid composition (e.g. as a result of alternative mRNA or premRNA processing, e.g. alternative splicing or limited proteolysis) and in addition, or in the alternative, may arise from differential post-translational modification (e.g., glycosylation, acylation, phosphorylation).

The term "modulate" when used herein in reference to expression or activity of a DPI or a DPI-related polypeptide refers to any change, e.g., upregulation or downregulation, of the expression or activity of the DPI or a DPI-related polypeptide. Based on the present disclosure, such modulation can be determined by assays known to those of skill in the art or described herein.

The percent identity of two amino acid sequences or of two nucleic acid sequences is determined by aligning the sequences for optimal comparison purposes(e.g., gaps can be introduced in the first sequence for best alignment with the sequence) and comparing the amino acid residues or nucleotides at corresponding positions. The "best alignment" is an alignment of two sequences which results in the highest percent identity. The percent identity is determined by the number of identical amino acid residues or nucleotides in the sequences being compared (i.e., % identity =# of identical positions/total # of positions x 100).

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm known to those of skill in the art. An example of a mathematical algorithm for comparing two sequences is the algorithm of Karlin and Altschul (1990) Proc. Natl. Acad. Sci. USA 87:2264-2268, modified as in Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5877. The NBLAST and XBLAST programs of Altschul, et al. (1990) J. Mol. Biol. 215:403-410 have incorporated such an algorithm. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (1997) Nucleic Acids Res. 25:3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules (Id.). When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See http://www.ncbi.nlm.nih.gov.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, CABIOS (1989). The ALIGN program (version 2.0) which is part of the GCG sequence alignment software package has incorporated such an algorithm. Other algorithms for sequence analysis known in the art include ADVANCE and ADAM as described in Torellis and Robotti (1994) Comput. Appl. Biosci., 10 :3-5; and FASTA described in Pearson and Lipman (1988) Proc. Natl. Acad. Sci. 85:2444-8. Within FASTA, ktup is a control option that sets the sensitivity and speed of the search.

4. BRIEF DESCRIPTION OF THE FIGURES

Figure 1 is an image obtained from 2-dimensional electrophoresis of normal CSF, which has been annotated to identify twelve landmark features, designated CSF1to CSF12.

Figure 2 shows the amino acid sequence of DPI-45 and DPI-213 (Figure 2B). The tryptic peptides identified by mass spectrometry are bold and italicized and the signal sequence is underlined. The nucleic acid sequence encoding the amino acid sequence of Figure 2B is shown in Figure 2A.

Figure 3 shows tissue distribution of DPI 45 and DPI-213 mRNA. Levels of mRNA in normal tissues were quantified by real time RT-PCR. mRNA levels are expressed as the number of copies per nanogram cDNA. Note the 50 times difference in scale between the left-hand part of the graph, containing brain-related samples, and the right-hand part of the graph, containing body samples.

5. DETAILED DESCRIPTION OF THE INVENTION

The invention described in detail below provides methods and compositions for clinical screening, diagnosis and prognosis of BAD in a mammalian subject, for monitoring the results of BAD therapy, for identifying patients most likely to respond to a particular therapeutic treatment and for drug screening and drug development. The invention also encompasses the administration of therapeutic compositions to a mammalian subject to treat or prevent BAD. The mammalian subject may be a non-human mammal, but is preferably human, more preferably a human adult, i.e. a human subject at least 21 (more preferably at least 35, at least 50, at least 60, at least 70, or at least 80) years old. For clarity of disclosure, and not by way of limitation, the invention will be described with respect to the analysis of CSF samples. However, as one skilled in the art will appreciate, based on the present description the assays and techniques described below can be applied to other types of samples, including a body fluid (e.g. blood, serum, plasma, saliva or urine), a tissue sample from a subject at risk of having or developing BAD (e.g. a biopsy such as a brain biopsy) or homogenate thereof. The methods and compositions of the present invention are useful for screening, diagnosis and prognosis of a living subject, but may also be used for postmortem diagnosis in a subject, for example, to identify family members of the subject who are at risk of developing the same disease.

As used herein, cerebrospinal fluid (CSF) refers to the fluid that surrounds the bulk of the central nervous system, as described in Physiological Basis of Medical Practice (J.B. West, ed., Williams and Wilkins, Baltimore, MD 1985). CSF includes ventricular CSF and lumbar CSF.

As used herein, the term "serum" refers to the supernatant fluid produced by clotting and centrifugal sedimentation of a blood sample. As used herein, the term "plasma" refers to the supernatant fluid produced by inhibition of clotting (for example, by citrate or EDTA) and centrifugal sedimentation of a blood sample. The term "blood" as used herein includes serum and plasma.

5.1 Depression-Associated Features (DFs)

In one aspect of the invention, two-dimensional electrophoresis is used to analyze CSF from a subject, preferably a living subject, in order to detect or quantify the expression of one or more Depression-Associated Features (DFs) for screening, prevention or diagnosis of BAD, to determine the prognosis of a subject having BAD, to monitor progression of BAD, to monitor the effectiveness of BAD therapy, for identifying patients most likely to respond to a particular therapeutic treatment, or for drug development. As used herein, "two-dimensional electrophoresis" (2D-electrophoresis) means a technique comprising isoelectric focusing, followed by denaturing electrophoresis; this generates a two-dimensional gel (2D-gel) containing a plurality of separated proteins. Preferably, the step of denaturing electrophoresis uses polyacrylamide electrophoresis in the presence of sodium dodecyl sulfate (SDS-PAGE). Especially preferred are the highly accurate and automatable methods and apparatus ("the Preferred Technology") described in International Application No.97GB3307 (published as WO 98/23950) and in U.S. Patent No. 6,064,754, both filed December 1, 1997, each of which is incorporated herein by reference in its entirety with particular reference to the protocol at pages 23-35. Briefly, the Preferred Technology provides efficient, computer-assisted methods and apparatus for identifying, selecting and characterizing biomolecules (e.g. proteins, including glycoproteins) in a biological sample. A two-dimensional array is generated by separating biomolecules on a two-dimensional gel according to their electrophoretic mobility and isoelectric point. A computer-generated digital profile of the array is generated, representing the identity, apparent molecular weight, isoelectric point, and relative abundance of a plurality of biomolecules detected in the two-dimensional

array, thereby permitting computer-mediated comparison of profiles from multiple biological samples, as well as computer aided excision of separated proteins of interest.

A preferred scanner for detecting fluorescently labeled proteins is described inWO 96/36882 and in the Ph.D. thesis of David A. Basiji, entitled "Development of a High-throughput Fluorescence Scanner Employing Internal Reflection Optics and Phase-sensitive Detection (Total Internal Reflection, Electrophoresis)", University of Washington (1997), Volume 58/12-B of Dissertation Abstracts International, page6686, the contents of each of which are incorporated herein by reference. These documents describe an image scanner designed specifically for automated, integrated operation at high speeds. The scanner can image gels that have been stained with fluorescent dyes or silver stains, as well as storage phosphor screens. The Basiji thesis provides a phase-sensitive detection system for discriminating modulated fluorescence from baseline noise due to laser scatter or homogeneous fluorescence, but the scanner can also be operated in a non-phase-sensitive mode. This phase-sensitive detection capability would increase the sensitivity of the instrument by an order of magnitude or more compared to conventional fluorescence imaging systems. The increased sensitivity would reduce the sample-preparation load on the upstream instruments while the enhanced image quality simplifies image analysis downstream in the process.

A more highly preferred scanner is the Apollo 2 scanner (Oxford Glycosciences, Oxford, UK), which is a modified version of the above described scanner. In the Apollo 2 scanner, the gel is transported through the scanner on a precision lead-screw drive system. This is preferable to laying the glass plate on the belt-driven system that is described in the Basiji thesis, as it provides a reproducible means of accurately transporting the gel past the imaging optics.

In the Apollo 2 scanner, the gel is secured against three alignment stops that rigidly hold the glass plate in a known position. By doing this in conjunction with the above precision transport system, the absolute position of the gel can be predicted and recorded. This ensures that co-ordinates of each feature on the gel can be determined more accurately and communicated, if desired, to a cutting robot for excision of the feature. In the Apollo 2 scanner, the carrier that holds the gel has four integral fluorescent markers for use to correct the image geometry. These markers are a quality control feature that confirms that the scanning has been performed correctly.

In comparison to the scanner described in the Basiji thesis, the optical components of the Apollo 2 scanner have been inverted. In the Apollo 2 scanner, the laser, mirror, waveguide and other optical components are above the glass plate being scanned. The scanner described in the Basiji thesis has these components underneath. In the Apollo 2 scanner, the glass plate is mounted onto the scanner gel side down, so that the optical path remains through the glass plate. By doing this, any particles of gel that may break away from the glass plate will fall onto the base of the instrument rather than into the optics. This does not affect the functionality of the system, but increases its reliability.

Still more preferred is the Apollo 3 scanner, in which the signal output is digitized to the full 16-bit data without any peak saturation or without square root encoding of the signal. A compensation algorithm has also been applied to correct for any variation in detection sensitivity along the path of the scanning beam. This variation is due to anomalies in the optics and differences in collection efficiency across the waveguide. A calibration is performed using a perspex plate with an even fluorescence throughout. The data received from a scan of this plate are used to determine the multiplication factors needed to increase the signal from each pixel level to a target level. These factors are then used in subsequent scans of gels to remove any internal optical variations.

As used herein, the term "feature" refers to a spot detected in a 2D gel, and the term "Depression-Associated Feature" (DF) refers to a feature that is differentially present in a sample (e.g. a sample of CSF) from a subject having BAD compared with a sample (e.g. a sample of CSF) from a subject free from BAD. As used herein, a feature (or a protein isoform of DPI, as defined infra) is "differentially present" in a first sample with respect to a second sample when a method for detecting the feature, isoform or DPI (e.g., 2D electrophoresis or an immunoassay) gives a different signal when applied to the first and second samples. A feature, isoform or DPI is "increased" in the first sample with respect to the second if the method of detection indicates that the feature, isoform or DPI is more abundant in the first sample than in the second sample, or if the feature, isoform or DPI is detectable in the first sample and undetectable in the second sample. Conversely, a feature, isoform or DPI is "decreased" in the first sample with respect to the second if the method of detection indicates that the feature, isoform or DPI is less abundant in the first sample than in

the second sample or if the feature, isoform or DPI is undetectable in the first sample and detectable in the second sample.

Preferably, the relative abundance of a feature in two samples is determined in two steps. First, the signal obtained upon detecting the feature in a sample is normalized by reference to a suitable background parameter, e.g., (a) to the total protein in the sample being analyzed (e.g., total protein loaded onto a gel); (b) to an Expression Reference Feature (ERF) i.e., a feature whose abundance is invariant, within the limits of variability of the Preferred Technology, in the population of subjects being examined, e.g. the ERFs disclosed below, or (c) more preferably to the total signal detected from all proteins in the sample.

Secondly, the normalized signal for the feature in one sample or sample set is compared with the normalized signal for the same feature in another sample or sample set in order to identify features that are "differentially present" in the first sample (or sample set) with respect to the second.

The DFs disclosed herein have been identified by comparing CSF samples from subjects having BAD against CSF samples from subjects free from BAD. Subjects free from BAD include subjects with no known disease or condition (normal subjects) and subjects with BAD.

Two groups of DFs have been identified through the methods and apparatus of the Preferred Technology. The first group consists of DFs that are decreased in the CSF of subjects having BAD as compared with the CSF of subjects free from BAD. These DFs can be described by apparent molecular weight (MW) and isoelectric point(pI) as provided in Table I.

Table I. DFs Decreased in CSF of Subjects Having BAD

DF#	pI	MW (Da)	Fold Decrease	Rank Sum - P value
DF-3	5.71	65446	52.34	
DF-4	4.82	155156	38.23	
DF-5	9.00	14098	36.14	
DF-6	9.05	18350	41.22	
DF-7	9.07	17183	28.50	
DF-8	7.18	20921	16.17	
DF-9	4.83	184426	14.37	
DF-10	4.93	27009	13.81	

DF-11	4.89	105482	10.85	
DF-12	6.62	175109	8.10	
DF-13	7.58	150536	8.32	
DF-14	4.55	24374	8.27	
DF-15	5.18	221724	7.27	
DF-16	5.74	131837	7.02	
DF-17	5.75	186832	6.10	
DF-18	4.29	62182	13.03	
DF-19	5.66	186832	5.09	
DF-20	6.49	44515	4.39	
DF-21	7.31	18459	5.25	
DF-22	4.47	54791	5.80	
DF-23	5.64	58495	8.45	
DF-24	4.86	153822	7.80	
DF-25	5.67	32549	5.13	0.01996
DF-26	3.94	48929	4.39	
DF-27	6.05	145133	3.68	
DF-28	9.59	68368	5.26	
DF-29	9.35	13879	4.58	
DF-30	5.02	80131	5.75	
DF-31	5.13	82859	5.19	0.01219
DF-32	5.65	12966	4.47	
DF-33	5.12	37524	4.00	
DF-34	8.14	13783	4.68	
DF-35	6.12	17901	3.72	
DF-36	9.04	11790	4.25	0.01219
DF-37	5.49	57515	6.01	
DF-39	4.37	102603	5.27	
DF-40	5.04	36196	4.78	
DF-41	4.64	146425	5.31	
DF-42	4.50	53966	3.51	0.01996
DF-43	9.86	34695	4.01	
DF-44	4.48	110040	4.55	
DF-47	5.88	146510	2.73	
DF-48	4.86	12080	5.34	
DF-51	5.98	90092	2.90	0.02157
DF-52	6.37	101661	3.12	0.01219
DF-55	5.67	48092	2.49	0.02157

DF-56	5.89	91613	2.23	0.03671
DF-58	4.77	91613	2.76	0.01945
DF-59	6.21	145638	2.11	
DF-60	6.05	47450	2.33	0.01219
DF-61	6.93	27331	2.12	0.01219
DF-64	4.50	61297	2.28	0.03038
DF-65	4.86	60009	2.56	0.01219
DF-66	7.10	23117	2.05	0.01219
DF-67	4.94	12681	2.17	0.03038
DF-68	9.18	39998	1.76	0.03671
DF-69	5.90	23795	1.84	0.02157
DF-70	4.91	38741	2.15	0.01219
DF-71	7.09	21231	1.75	0.02157
DF-170	9.05	19478	31.66	
DF-171	4.88	154564	22.67	
DF-172	4.29	53154	17.63	
DF-173	5.05	153158	15.01	
DF-174	5.59	56791	13.00	
DF-175	8.38	33742	11.85	
DF-176	4.47	128027	11.16	
DF-177	8.01	20872	10.37	
DF-178	8.17	12814	10.13	
DF-179	4.63	33899	8.69	
DF-180	5.68	50944	8.33	
DF-181	6.21	188454	7.20	
DF-182	4.86	169810	6.83	
DF-183	5.99	146471	5.94	
DF-184	4.64	110461	4.51	
DF-185	6.10	11823	4.47	
DF-186	4.78	82859	4.41	
DF-187	6.08	63191	4.35	
DF-188	4.31	63376	4.27	
DF-189	9.05	19032	4.18	
DF-190	4.55	109447	4.08	
DF-191	6.30	186832	3.90	
DF-192	4.70	83322	3.83	0.03689
DF-193	4.67	14570	3.70	0.03689
DF-194	4.57	30225	3.42	

DF-195	4.98	157461	2.92	
DF-196	4.63	11114	2.41	
DF-197	4.40	27223	2.32	
DF-198	7.89	57515	2.25	
DF-199	6.86	60862	2.21	
DF-200	6.34	20539	2.20	0.03389
DF-201	6.89	31721	2.13	
DF-202	6.30	23117	2.08	
DF-203	4.70	37742	2.06	0.02157
DF-204	4.46	32643	1.96	0.03038
DF-205	5.33	18229	1.86	0.03615
DF-206	4.36	12420	1.84	
DF-207	5.95	13129	1.83	0.03671
DF-208	8.16	24182	1.74	0.03671
DF-209	4.57	13499	1.73	0.01996
DF-210	5.37	123390	1.71	0.03671
DF-211	4.72	20882	1.70	0.02157
DF-212	9.41	17233	1.64	
DF-213	5.19	48827	1.60	
DF-214	4.51	102603	1.58	
DF-215	5.04	57690	1.53	0.02157
DF-216	5.03	39080	1.37	
DF-217	4.53	36239	1.36	
DF-218	4.74	30882	1.31	
DF-219	4.70	186027	1.28	
DF-220	4.31	47931	1.27	
DF-221	7.26	16614	1.26	
DF-222	4.69	156503	1.25	
DF-223	5.91	99384	1.19	
DF-224	6.10	184426	1.14	
DF-225	4.41	24762	1.08	
DF-226	5.08	26332	1.07	
DF-227	6.06	184426	1.01	
DF-228	5.48	51880	1.01	
DF-229	5.28	58608	1.00	

Where p values are given in Table I, the statistical technique used was the Wilcoxon Rank-Sum test as described in method (a) of Section 6.1.13, Statistical

Analysis of the Profiles. Where no p value is reported, the method used to select these features was on the basis of a significant fold change or qualitative presence or absence alone as described in methods (b) and (c) of Section 6.1.13 Statistical Analysis of the Profiles.

The second group consists of DFs that are increased in the CSF of subjects having BAD as compared with the CSF of subjects free from BAD. These DFs can be described by apparent molecular weight (MW) and isoelectric point (pI) as provided in Table II.

Table II. DFs Increased in CSF of Subjects Having BAD

DF#	pI	MW (Da)	Fold Increase	Rank Sum - P value
DF-76	7.24	11749	91.68	
DF-77	7.09	27075	> 100	
DF-78	9.01	10999	> 100	
DF-82	6.61	11467	> 100	
DF-84	7.98	11312	15.72	
DF-86	4.86	28850	> 100	
DF-87	6.92	11749	> 100	
DF-94	7.48	11668	> 100	
DF-95	7.05	11388	> 100	
DF-96	7.48	11932	90.70	
DF-97	6.65	11872	36.46	
DF-98	6.46	12064	68.12	
DF-99	6.28	10506	32.49	
DF-100	7.01	57356	30.55	
DF-101	6.80	32080	31.65	
DF-102	7.31	11037	51.36	
DF-103	5.50	20607	36.83	
DF-104	4.64	10735	1.02	
DF-105	6.62	39221	16.68	
DF-106	4.59	40613	1.06	
DF-107	5.88	10560	17.09	
DF-108	6.00	11753	17.02	
DF-109	9.38	51133	21.21	
DF-110	6.39	12122	15.81	0.01996
DF-111	4.97	20607	7.45	0.01996
DF-112	7.42	43773	6.15	0.02157

DF-113	6.36	27116	6.13	0.03038
DF-115	5.59	39882	2.04	0.02940
DF-117	5.76	39054	2.70	0.03734
DF-118	7.81	43773	3.87	0.01219
DF-120	7.01	40510	3.83	0.01219
DF-121	6.42	32454	2.75	0.01219
DF-123	5.19	12080	3.21	0.03671
DF-124	5.54	21908	3.39	0.01996
DF-125	6.18	43043	2.90	0.02157
DF-126	6.34	25658	2.83	0.01219
DF-127	7.85	45269	2.39	0.01996
DF-130	7.27	48975	3.03	0.01219
DF-131	5.79	39536	2.12	0.03615
DF-132	6.46	35925	2.24	0.03671
DF-134	6.39	44664	2.04	0.03671
DF-135	5.30	43920	2.68	0.01219
DF-137	6.66	19935	1.84	0.01996
DF-138	5.01	43626	3.08	0.01219
DF-141	5.05	20268	2.07	0.03671
DF-142	5.10	46974	2.53	0.01219
DF-144	4.62	28747	2.05	0.01996
DF-145	6.53	10226	2.11	0.01996
DF-146	5.03	46659	2.19	0.03671
DF-148	6.29	80131	2.41	0.03671
DF-153	4.95	44515	2.15	0.02157
DF-155	7.03	155828	1.92	0.01794
DF-158	7.70	40407	1.87	0.03734
DF-161	6.88	40613	1.86	0.03671
DF-164	4.96	74524	1.52	0.01219
DF-230	7.20	9982	45.46	
DF-231	7.02	33025	42.27	
DF-232	6.60	11945	30.47	
DF-233	9.86	49588	30.06	
DF-234	4.91	24530	29.31	
DF-235	9.75	11627	26.60	
DF-236	7.05	32024	19.72	
DF-237	6.69	39193	18.60	
DF-238	5.77	11076	18.25	

DF-239	5.73	22738	17.21	
DF-240	4.86	148596	16.16	
DF-241	6.31	43188	15.59	
DF-242	5.34	67000	14.99	
DF-243	7.92	68295	14.65	
DF-244	5.21	114613	14.28	
DF-245	6.69	34705	14.09	
DF-246	5.66	12246	13.92	
DF-247	6.15	54088	13.90	
DF-248	4.67	35945	13.90	
DF-249	9.81	41481	13.83	
DF-250	7.18	41192	13.57	
DF-251	6.89	57760	13.52	
DF-252	6.93	12686	13.26	
DF-253	7.28	42470	13.02	
DF-254	7.57	21302	13.02	
DF-255	5.86	11775	12.96	
DF-256	7.27	35119	12.59	
DF-257	6.78	11955	11.94	
DF-258	6.30	44664	11.81	
DF-259	9.76	15407	11.59	
DF-260	8.78	54716	11.54	
DF-261	4.17	40285	11.47	
DF-262	7.44	26066	10.66	
DF-263	7.60	43250	10.58	
DF-264	7.03	42468	10.54	
DF-265	7.81	24686	10.47	
DF-266	6.45	20882	10.42	
DF-267	7.70	142870	10.14	
DF-268	9.13	50939	10.00	
DF-269	5.00	31104	9.96	
DF-270	4.16	106117	9.87	
DF-271	9.58	21021	9.76	
DF-272	7.88	20262	9.30	
DF-273	5.60	12917	9.26	
DF-274	5.81	11746	9.17	
DF-275	6.23	12206	9.09	
DF-276	5.85	39763	9.09	

DF-277	4.31	13863	8.98	
DF-278	6.39	36929	8.83	
DF-279	6.10	35904	8.64	
DF-280	5.64	43225	8.47	
DF-281	6.48	31008	8.39	
DF-282	5.98	45728	8.35	
DF-283	9.24	11400	8.28	
DF-284	5.61	114691	8.26	
DF-285	7.80	42224	8.22	
DF-286	6.11	12038	7.92	
DF-287	9.59	22365	7.85	
DF-288	5.00	29267	7.70	
DF-289	5.58	32266	6.82	0.03038
DF-290	6.69	27128	6.81	0.03038
DF-291	8.79	23405	5.69	
DF-292	6.82	41791	5.34	0.03689
DF-293	6.26	11675	5.33	
DF-294	6.21	41342	5.17	
DF-295	8.54	54625	5.12	
DF-296	5.50	112518	4.76	
DF-297	5.49	15277	4.49	
DF-298	6.43	45269	4.46	0.03038
DF-299	7.15	15381	4.15	
DF-300	4.94	16019	4.04	
DF-301	9.58	20268	3.77	0.03689
DF-302	7.28	34494	3.26	
DF-303	7.48	59646	3.22	0.03671
DF-304	6.71	43920	3.12	
DF-305	5.71	122257	3.08	
DF-306	6.36	24567	2.84	0.04975
DF-307	5.83	111485	2.81	
DF-308	4.96	47897	2.70	
DF-309	4.99	11955	2.66	
DF-310	5.53	142313	2.58	
DF-311	6.16	35402	2.40	0.04360
DF-312	6.24	136566	2.39	
DF-313	5.50	80131	2.36	0.03689
DF-314	5.55	113560	2.35	

DF-315	7.51	37524	2.29	
DF-316	5.43	43086	2.29	
DF-317	7.84	142929	2.28	
DF-318	6.20	54527	2.24	
DF-319	6.81	51880	2.18	0.03689
DF-320	4.63	31440	2.13	0.03689
DF-321	6.66	65725	2.05	0.03038
DF-322	8.79	22458	2.05	
DF-323	6.57	21549	1.83	
DF-324	5.64	41761	1.82	0.04975
DF-325	9.71	17798	1.80	
DF-326	5.82	41902	1.78	
DF-327	5.22	13359	1.77	0.03671
DF-328	7.41	52456	1.76	
DF-329	4.19	20607	1.71	
DF-330	5.54	37852	1.67	0.03615
DF-331	8.11	57515	1.67	
DF-332	6.34	53167	1.66	
DF-333	5.49	38854	1.64	0.03689
DF-334	4.44	37962	1.64	
DF-335	4.83	55426	1.55	
DF-336	6.60	29689	1.54	
DF-337	5.83	27935	1.53	
DF-338	4.37	40820	1.48	
DF-339	4.47	91103	1.47	
DF-340	7.50	20201	1.47	
DF-341	5.25	178771	1.47	
DF-342	5.12	15174	1.44	
DF-343	5.42	18290	1.42	
DF-344	4.35	41481	1.40	
DF-345	4.84	20744	1.40	
DF-346	6.04	43920	1.38	
DF-347	4.93	25356	1.37	
DF-348	6.28	48238	1.35	
DF-349	5.84	65031	1.33	
DF-350	4.34	10961	1.31	
DF-351	9.07	23405	1.25	
DF-352	6.58	93680	1.19	

DF-353	5.36	28921	1.19	
DF-354	6.11	12903	1.15	
DF-355	6.18	187641	1.13	
DF-356	4.93	102603	1.06	
DF-357	7.02	70955	1.03	
DF-358	4.95	45574	1.01	

Where p values are given in Table II, the statistical technique used was the Wilcoxon Rank-Sum test as described in method (a) of Section 6.1.13, Statistical Analysis of the Profiles. Where no p value is reported, the method used to select these features was on the basis of a significant fold change or qualitative presence or absence alone as described in methods (b) and (c) of Section 6.1.13 Statistical Analysis of the Profiles.

For any given DF, the signal obtained upon analyzing CSF from subjects having BAD relative to the signal obtained upon analyzing CSF from subjects free from BAD will depend upon the particular analytical protocol and detection technique that is used. Accordingly, the present invention contemplates that each laboratory will, based on the present description, establish a reference range for each DF in subjects free from BAD according to the analytical protocol and detection technique in use, as is conventional in the diagnostic art. Preferably, at least one positive control CSF sample from a subject known to have BAD or at least one negative control CSF sample from a subject known to be free from BAD (and more preferably both positive and negative control samples) are included in each batch of test samples analyzed. In one embodiment, the level of expression of a feature is determined relative to a background value, which is defined as the level of signal obtained from a proximal region of the image that (a) is equivalent in area to the particular feature in question; and (b) contains no discernable protein feature. The reference range, depending upon the method of detection used and the conditions under which detection is carried out, can include no feature or isoform present, or non-detectable levels of feature or isoform present. Proteins described by pI and MW provided in Tables I and II can be identified by searching 2D-PAGE databases with those pI and MW values. Examples of such databases are provided on the ExPASy Molecular Biology Server (http://www.expasy.ch) under the "SWISS-2DPAGE" section, and other databases are further referenced on this server. Such databases typically provide interactive 2D gels

images for a given set of sample and preparation protocol, and the skilled artisan can obtain information relevant to a given feature by pointing and clicking the appropriate section of the image.

In a preferred embodiment, the signal associated with an DF in the CSF of a subject (e.g., a subject suspected of having or known to have BAD) is normalized with reference to one or more ERFs detected in the same 2D gel. As will be apparent to one of ordinary skill in the art, such ERFs may readily be determined by comparing different samples using the Preferred Technology. Suitable ERFs include (but are not limited to) that described in the following table.

Table III. Expression Reference Features

ERF#	Molecular Weight (Da)	pI
ERF-1	79685	5.87
ERF-2	74524	4.96

As those of skill in the art will readily appreciate, the measured MW and pI of a given feature or protein isoform will vary to some extent depending on the precise protocol used for each step of the 2D electrophoresis and for landmark matching. As used herein, the terms "MW" and "pI" are defined, respectively, to mean the apparent molecular weight in Daltons and the apparent isoelectric point of a feature or protein isoform as measured in exact accordance with the Reference Protocol identified in Section 6 below. When the Reference Protocol is followed and when samples are run in duplicate or a higher number of replicates, variation in the measured mean pI of a DF or DPI is typically less than 3% and variation in the measured mean MW of a DF or DPI is typically less than 5%. Where the skilled artisan wishes to deviate from the Reference Protocol, calibration experiments should be performed to compare the MW and pI for each DF or protein isoform as detected (a) by the Reference Protocol and (b) by the deviant protocol. Proteins described by pI and MW provided in Tables I and II can be identified by searching 2D-PAGE databases with those pI and MW values. Examples of such databases are provided on the ExPASy Molecular Biology Server (http://www.expasy.ch) under the "SWISS-2DPAGE" section, and other databases are further referenced on this server. Such databases typically provide interactive 2D gels images for a given set of sample and preparation protocol, and the

skilled artisan can obtain information relevant to a given feature by pointing and clicking the appropriate section of the image.

DFs can be used for detection, prognosis, diagnosis, or monitoring of BAD or for drug development. In one embodiment of the invention, CSF from a subject (e.g., a subject suspected of having BAD) is analyzed by 2D electrophoresis for quantitative detection of one or more of the following DFs: DF-3, DF-4, DF-5, DF-6, DF-7, DF-8, DF-9, DF-10, DF-11, DF-12, DF-13, DF-14, DF-15, DF-16, DF-17, DF-18, DF-19, DF-20, DF-21, DF-22, DF-23, DF-24, DF-25, DF-26, DF-27, DF-28, DF-29, DF-30, DF-31, DF-32, DF-33, DF-34, DF-35, DF-36, DF-37, DF-39, DF-40, DF-41, DF-42, DF-43, DF-44, DF-47, DF-48, DF-51, DF-52, DF-55, DF-56, DF-58, DF-59, DF-60, DF-61, DF-64, DF-65, DF-66, DF-67, DF-68, DF-69, DF-70, DF-71, DF-170, DF-171, DF-172, DF-173, DF-174, DF-175, DF-176, DF-177, DF-178, DF-179, DF-180, DF-181, DF-182, DF-183, DF-184, DF-185, DF-186, DF-187, DF-188, DF-189, DF-190, DF-191, DF-192, DF-193, DF-194, DF-195, DF-196, DF-197, DF-198, DF-199, DF-200, DF-201, DF-202, DF-203, DF-204, DF-205, DF-206, DF-207, DF-208, DF-209, DF-210, DF-211, DF-212, DF-213, DF-214, DF-215, DF-216, DF-217, DF-218, DF-219, DF-220, DF-221, DF-222, DF-223, DF-224, DF-225, DF-226, DF-227, DF-228, DF-229. A decreased abundance of said one or more DFs in the CSF from the subject relative to CSF from a subject or subjects free from BAD (e.g., a control sample or a previously determined reference range) indicates the presence of BAD.

In another embodiment of the invention, CSF from a subject is analyzed by 2D electrophoresis for quantitative detection of one or more of the following DFs: DF-76, DF-77, DF-78, DF-82, DF-84, DF-86, DF-87, DF-94, DF-95, DF-96, DF-97, DF-98, DF-99, DF-100, DF-101, DF-102, DF-103, DF-104, DF-105, DF-106, DF-107, DF-108, DF-109, DF-110, DF-111, DF-112, DF-113, DF-115, DF-117, DF-118, DF-120, DF-121, DF-123, DF-124, DF-125, DF-126, DF-127, DF-130, DF-131, DF-132, DF-134, DF-135, DF-137, DF-138, DF-141, DF-142, DF-144, DF-145, DF-146, DF-148, DF-153, DF-155, DF-158, DF-161, DF-164, DF-230, DF-231, DF-232, DF-233, DF-234, DF-235, DF-236, DF-237, DF-238, DF-239, DF-240, DF-241, DF-242, DF-243, DF-244, DF-245, DF-246, DF-247, DF-248, DF-249, DF-250, DF-251, DF-252, DF-253, DF-254, DF-255, DF-256, DF-257, DF-258, DF-259, DF-260, DF-261, DF-262, DF-263, DF-264, DF-265, DF-266, DF-267, DF-268, DF-269, DF-270, DF-271, DF-272, DF-273, DF-274, DF-275, DF-276, DF-277, DF-278, DF-279, DF-280, DF-281, DF-282, DF-283, DF-284, DF-285, DF-286, DF-287, DF-288, DF-289, DF-290, DF-

291, DF-292, DF-293, DF-294, DF-295, DF-296, DF-297, DF-298, DF-299, DF-300, DF-301, DF-302, DF-303, DF-304, DF-305, DF-306, DF-307, DF-308, DF-309, DF-310, DF-311, DF-312, DF-313, DF-314, DF-315, DF-316, DF-317, DF-318, DF-319, DF-320, DF-321, DF-322, DF-323, DF-324, DF-325, DF-326, DF-327, DF-328, DF-329, DF-330, DF-331, DF-332, DF-333, DF-334, DF-335, DF-336, DF-337, DF-338, DF-339, DF-340, DF-341, DF-342, DF-343, DF-344, DF-345, DF-346, DF-347, DF-348, DF-349, DF-350, DF-351, DF-352, DF-353, DF-354, DF-355, DF-356, DF-357, DF-358. An increased abundance of said one or more DFs in the CSF from the subject relative to CSF from a subject or subjects free from BAD (e.g., a control sample or a previously determined reference range) indicates the presence of BAD.

In yet another embodiment, CSF from a subject is analyzed by 2D electrophoresis for quantitative detection of (a) one or more DFs or any combination of them, whose decreased abundance indicates the presence of BAD, i.e., DF-3, DF-4, DF-5, DF-6, DF-7, DF-8, DF-9, DF-10, DF-11, DF-12, DF-13, DF-14, DF-15, DF-16, DF-17, DF-18, DF-19, DF-20, DF-21, DF-22, DF-23, DF-24, DF-25, DF-26, DF-27, DF-28, DF-29, DF-30, DF-31, DF-32, DF-33, DF-34, DF-35, DF-36, DF-37, DF-39, DF-40, DF-41, DF-42, DF-43, DF-44, DF-47, DF-48, DF-51, DF-52, DF-55, DF-56, DF-58, DF-59, DF-60, DF-61, DF-64, DF-65, DF-66, DF-67, DF-68, DF-69, DF-70, DF-71, DF-170, DF-171, DF-172, DF-173, DF-174, DF-175, DF-176, DF-177, DF-178, DF-179, DF-180, DF-181, DF-182, DF-183, DF-184, DF-185, DF-186, DF-187, DF-188, DF-189, DF-190, DF-191, DF-192, DF-193, DF-194, DF-195, DF-196, DF-197, DF-198, DF-199, DF-200, DF-201, DF-202, DF-203, DF-204, DF-205, DF-206, DF-207, DF-208, DF-209, DF-210, DF-211, DF-212, DF-213, DF-214, DF-215, DF-216, DF-217, DF-218, DF-219, DF-220, DF-221, DF-222, DF-223, DF-224, DF-225, DF-226, DF-227, DF-228, DF-229 and (b) one or more DFs or any combination of them, whose increased abundance indicates the presence of BAD i.e., DF-76, DF-77, DF-78, DF-82, DF-84, DF-86, DF-87, DF-94, DF-95, DF-96, DF-97, DF-98, DF-99, DF-100, DF-101, DF-102, DF-103, DF-104, DF-105, DF-106, DF-107, DF-108, DF-109, DF-110, DF-111, DF-112, DF-113, DF-115, DF-117, DF-118, DF-120, DF-121, DF-123, DF-124, DF-125, DF-126, DF-127, DF-130, DF-131, DF-132, DF-134, DF-135, DF-137, DF-138, DF-141, DF-142, DF-144, DF-145, DF-146, DF-148, DF-153, DF-155, DF-158, DF-161, DF-164, DF-230, DF-231, DF-232, DF-233, DF-234, DF-235, DF-236, DF-237, DF-238, DF-239, DF-240, DF-241, DF-242, DF-243, DF-244, DF-245, DF-246, DF-247, DF-248, DF-249, DF-250, DF-251, DF-252, DF-253, DF-

254, DF-255, DF-256, DF-257, DF-258, DF-259, DF-260, DF-261, DF-262, DF-263, DF-264, DF-265, DF-266, DF-267, DF-268, DF-269, DF-270, DF-271, DF-272, DF-273, DF-274, DF-275, DF-276, DF-277, DF-278, DF-279, DF-280, DF-281, DF-282, DF-283, DF-284, DF-285, DF-286, DF-287, DF-288, DF-289, DF-290, DF-291, DF-292, DF-293, DF-294, DF-295, DF-296, DF-297, DF-298, DF-299, DF-300, DF-301, DF-302, DF-303, DF-304, DF-305, DF-306, DF-307, DF-308, DF-309, DF-310, DF-311, DF-312, DF-313, DF-314, DF-315, DF-316, DF-317, DF-318, DF-319, DF-320, DF-321, DF-322, DF-323, DF-324, DF-325, DF-326, DF-327, DF-328, DF-329, DF-330, DF-331, DF-332, DF-333, DF-334, DF-335, DF-336, DF-337, DF-338, DF-339, DF-340, DF-341, DF-342, DF-343, DF-344, DF-345, DF-346, DF-347, DF-348, DF-349, DF-350, DF-351, DF-352, DF-353, DF-354, DF-355, DF-356, DF-357, DF-358.

In yet another embodiment of the invention, CSF from a subject is analyzed by 2D electrophoresis for quantitative detection of one or more of the following DFs: DF-3, DF-4, DF-5, DF-6, DF-7, DF-8, DF-9, DF-10, DF-11, DF-12, DF-13, DF-14, DF-15, DF-16, DF-17, DF-18, DF-19, DF-20, DF-21, DF-22, DF-23, DF-24, DF-25, DF-26, DF-27, DF-28, DF-29, DF-30, DF-31, DF-32, DF-33, DF-34, DF-35, DF-36, DF-37, DF-39, DF-40, DF-41, DF-42, DF-43, DF-44, DF-47, DF-48, DF-51, DF-52, DF-55, DF-56, DF-58, DF-59, DF-60, DF-61, DF-64, DF-65, DF-66, DF-67, DF-68, DF-69, DF-70, DF-71, DF-76, DF-77, DF-78, DF-82, DF-84, DF-86, DF-87, DF-94, DF-95, DF-96, DF-97, DF-98, DF-99, DF-100, DF-101, DF-102, DF-103, DF-104, DF-105, DF-106, DF-107, DF-108, DF-109, DF-110, DF-111, DF-112, DF-113, DF-115, DF-117, DF-118, DF-120, DF-121, DF-123, DF-124, DF-125, DF-126, DF-127, DF-130, DF-131, DF-132, DF-134, DF-135, DF-137, DF-138, DF-141, DF-142, DF-144, DF-145, DF-146, DF-148, DF-153, DF-155, DF-158, DF-161, DF-164, DF-170, DF-171, DF-172, DF-173, DF-174, DF-175, DF-176, DF-177, DF-178, DF-179, DF-180, DF-181, DF-182, DF-183, DF-184, DF-185, DF-186, DF-187, DF-188, DF-189, DF-190, DF-191, DF-192, DF-193, DF-194, DF-195, DF-196, DF-197, DF-198, DF-199, DF-200, DF-201, DF-202, DF-203, DF-204, DF-205, DF-206, DF-207, DF-208, DF-209, DF-210, DF-211, DF-212, DF-213, DF-214, DF-215, DF-216, DF-217, DF-218, DF-219, DF-220, DF-221, DF-222, DF-223, DF-224, DF-225, DF-226, DF-227, DF-228, DF-229, DF-230, DF-231, DF-232, DF-233, DF-234, DF-235, DF-236, DF-237, DF-238, DF-239, DF-240, DF-241, DF-242, DF-243, DF-244, DF-245, DF-246, DF-247, DF-248, DF-249, DF-250, DF-251, DF-252, DF-253, DF-254, DF-255, DF-256, DF-257, DF-258, DF-259, DF-260, DF-261, DF-262, DF-263, DF-264, DF-265,

DF-266, DF-267, DF-268, DF-269, DF-270, DF-271, DF-272, DF-273, DF-274, DF-275, DF-276, DF-277, DF-278, DF-279, DF-280, DF-281, DF-282, DF-283, DF-284, DF-285, DF-286, DF-287, DF-288, DF-289, DF-290, DF-291, DF-292, DF-293, DF-294, DF-295, DF-296, DF-297, DF-298, DF-299, DF-300, DF-301, DF-302, DF-303, DF-304, DF-305, DF-306, DF-307, DF-308, DF-309, DF-310, DF-311, DF-312, DF-313, DF-314, DF-315, DF-316, DF-317, DF-318, DF-319, DF-320, DF-321, DF-322, DF-323, DF-324, DF-325, DF-326, DF-327, DF-328, DF-329, DF-330, DF-331, DF-332, DF-333, DF-334, DF-335, DF-336, DF-337, DF-338, DF-339, DF-340, DF-341, DF-342, DF-343, DF-344, DF-345, DF-346, DF-347, DF-348, DF-349, DF-350, DF-351, DF-352, DF-353, DF-354, DF-355, DF-356, DF-357, DF-358 wherein the ratio of the one or more DFs relative to an Expression Reference Feature (ERF) indicates whether BAD is present. In a specific embodiment, a decrease in one or more DF/ERF ratios in a test sample relative to the DF/ERF ratios in a control sample or a reference range indicates the presence of BAD; DF-3, DF-4, DF-5, DF-6, DF-7, DF-8, DF-9, DF-10, DF-11, DF-12, DF-13, DF-14, DF-15, DF-16, DF-17, DF-18, DF-19, DF-20, DF-21, DF-22, DF-23, DF-24, DF-25, DF-26, DF-27, DF-28, DF-29, DF-30, DF-31, DF-32, DF-33, DF-34, DF-35, DF-36, DF-37, DF-39, DF-40, DF-41, DF-42, DF-43, DF-44, DF-47, DF-48, DF-51, DF-52, DF-55, DF-56, DF-58, DF-59, DF-60, DF-61, DF-64, DF-65, DF-66, DF-67, DF-68, DF-69, DF-70, DF-71, DF-170, DF-171, DF-172, DF-173, DF-174, DF-175, DF-176, DF-177, DF-178, DF-179, DF-180, DF-181, DF-182, DF-183, DF-184, DF-185, DF-186, DF-187, DF-188, DF-189, DF-190, DF-191, DF-192, DF-193, DF-194, DF-195, DF-196, DF-197, DF-198, DF-199, DF-200, DF-201, DF-202, DF-203, DF-204, DF-205, DF-206, DF-207, DF-208, DF-209, DF-210, DF-211, DF-212, DF-213, DF-214, DF-215, DF-216, DF-217, DF-218, DF-219, DF-220, DF-221, DF-222, DF-223, DF-224, DF-225, DF-226, DF-227, DF-228, DF-229 are suitable DFs for this purpose. In another specific embodiment, an increase in one or more DF/ERF ratios in a test sample relative to the DF/ERF ratios in a control sample or a reference range indicates the presence of BAD; DF-76, DF-77, DF-78, DF-82, DF-84, DF-86, DF-87, DF-94, DF-95, DF-96, DF-97, DF-98, DF-99, DF-100, DF-101, DF-102, DF-103, DF-104, DF-105, DF-106, DF-107, DF-108, DF-109, DF-110, DF-111, DF-112, DF-113, DF-115, DF-117, DF-118, DF-120, DF-121, DF-123, DF-124, DF-125, DF-126, DF-127, DF-130, DF-131, DF-132, DF-134, DF-135, DF-137, DF-138, DF-141, DF-142, DF-144, DF-145, DF-146, DF-148, DF-153, DF-155, DF-158, DF-161, DF-164, DF-230, DF-231, DF-232, DF-233, DF-234,

DF-235, DF-236, DF-237, DF-238, DF-239, DF-240, DF-241, DF-242, DF-243, DF-244, DF-245, DF-246, DF-247, DF-248, DF-249, DF-250, DF-251, DF-252, DF-253, DF-254, DF-255, DF-256, DF-257, DF-258, DF-259, DF-260, DF-261, DF-262, DF-263, DF-264, DF-265, DF-266, DF-267, DF-268, DF-269, DF-270, DF-271, DF-272, DF-273, DF-274, DF-275, DF-276, DF-277, DF-278, DF-279, DF-280, DF-281, DF-282, DF-283, DF-284, DF-285, DF-286, DF-287, DF-288, DF-289, DF-290, DF-291, DF-292, DF-293, DF-294, DF-295, DF-296, DF-297, DF-298, DF-299, DF-300, DF-301, DF-302, DF-303, DF-304, DF-305, DF-306, DF-307, DF-308, DF-309, DF-310, DF-311, DF-312, DF-313, DF-314, DF-315, DF-316, DF-317, DF-318, DF-319, DF-320, DF-321, DF-322, DF-323, DF-324, DF-325, DF-326, DF-327, DF-328, DF-329, DF-330, DF-331, DF-332, DF-333, DF-334, DF-335, DF-336, DF-337, DF-338, DF-339, DF-340, DF-341, DF-342, DF-343, DF-344, DF-345, DF-346, DF-347, DF-348, DF-349, DF-350, DF-351, DF-352, DF-353, DF-354, DF-355, DF-356, DF-357, DF-358 are suitable DFs for this purpose.

In a further embodiment of the invention, CSF from a subject is analyzed by 2D electrophoresis for quantitative detection of (a) one or more DFs, or any combination of them, whose decreased DF/ERF ratio(s) in a test sample relative to the DF/ERF ratio(s) in a control sample indicates the presence of BAD, i.e., DF-3, DF-4, DF-5, DF-6, DF-7, DF-8, DF-9, DF-10, DF-11, DF-12, DF-13, DF-14, DF-15, DF-16, DF-17, DF-18, DF-19, DF-20, DF-21, DF-22, DF-23, DF-24, DF-25, DF-26, DF-27, DF-28, DF-29, DF-30, DF-31, DF-32, DF-33, DF-34, DF-35, DF-36, DF-37, DF-39, DF-40, DF-41, DF-42, DF-43, DF-44, DF-47, DF-48, DF-51, DF-52, DF-55, DF-56, DF-58, DF-59, DF-60, DF-61, DF-64, DF-65, DF-66, DF-67, DF-68, DF-69, DF-70, DF-71, DF-170, DF-171, DF-172, DF-173, DF-174, DF-175, DF-176, DF-177, DF-178, DF-179, DF-180, DF-181, DF-182, DF-183, DF-184, DF-185, DF-186, DF-187, DF-188, DF-189, DF-190, DF-191, DF-192, DF-193, DF-194, DF-195, DF-196, DF-197, DF-198, DF-199, DF-200, DF-201, DF-202, DF-203, DF-204, DF-205, DF-206, DF-207, DF-208, DF-209, DF-210, DF-211, DF-212, DF-213, DF-214, DF-215, DF-216, DF-217, DF-218, DF-219, DF-220, DF-221, DF-222, DF-223, DF-224, DF-225, DF-226, DF-227, DF-228, DF-229; (b) one or more DFs, or any combination of them, whose increased DF/ERF ratio(s) in a test sample relative to the DF/ERF ratio(s) in a control sample indicates the presence of BAD, i.e., DF-76, DF-77, DF-78, DF-82, DF-84, DF-86, DF-87, DF-94, DF-95, DF-96, DF-97, DF-98, DF-99, DF-100, DF-101, DF-102, DF-103, DF-104, DF-105, DF-106, DF-107, DF-108, DF-109, DF-110,

DF-111, DF-112, DF-113, DF-115, DF-117, DF-118, DF-120, DF-121, DF-123, DF-124, DF-125, DF-126, DF-127, DF-130, DF-131, DF-132, DF-134, DF-135, DF-137, DF-138, DF-141, DF-142, DF-144, DF-145, DF-146, DF-148, DF-153, DF-155, DF-158, DF-161, DF-164, DF-230, DF-231, DF-232, DF-233, DF-234, DF-235, DF-236, DF-237, DF-238, DF-239, DF-240, DF-241, DF-242, DF-243, DF-244, DF-245, DF-246, DF-247, DF-248, DF-249, DF-250, DF-251, DF-252, DF-253, DF-254, DF-255, DF-256, DF-257, DF-258, DF-259, DF-260, DF-261, DF-262, DF-263, DF-264, DF-265, DF-266, DF-267, DF-268, DF-269, DF-270, DF-271, DF-272, DF-273, DF-274, DF-275, DF-276, DF-277, DF-278, DF-279, DF-280, DF-281, DF-282, DF-283, DF-284, DF-285, DF-286, DF-287, DF-288, DF-289, DF-290, DF-291, DF-292, DF-293, DF-294, DF-295, DF-296, DF-297, DF-298, DF-299, DF-300, DF-301, DF-302, DF-303, DF-304, DF-305, DF-306, DF-307, DF-308, DF-309, DF-310, DF-311, DF-312, DF-313, DF-314, DF-315, DF-316, DF-317, DF-318, DF-319, DF-320, DF-321, DF-322, DF-323, DF-324, DF-325, DF-326, DF-327, DF-328, DF-329, DF-330, DF-331, DF-332, DF-333, DF-334, DF-335, DF-336, DF-337, DF-338, DF-339, DF-340, DF-341, DF-342, DF-343, DF-344, DF-345, DF-346, DF-347, DF-348, DF-349, DF-350, DF-351, DF-352, DF-353, DF-354, DF-355, DF-356, DF-357, DF-358.

In a preferred embodiment, CSF from a subject is analyzed for quantitative detection of a plurality of DFs.

5.2 Depression-Associated Protein Isoforms (DPIs)

In another aspect of the invention, CSF from a subject, preferably a living subject, is analyzed for quantitative detection of one or more Depression-Associated Protein Isoforms (DPIs) for screening or diagnosis of BAD, to determine the prognosis of a subject having BAD, to monitor the effectiveness of BAD therapy, for identifying patients most likely to respond to a particular therapeutic treatment or for drug development. As is well known in the art, a given protein may be expressed as variants (isoforms) that differ in their amino acid composition (e.g. as a result of alternative mRNA or premRNA processing, e.g. alternative splicing or limited proteolysis) or as a result of differential post-translational modification (e.g., glycosylation, phosphorylation, acylation), or both, so that proteins of identical amino acid sequence can differ in their pI, MW, or both. It follows that differential presence of a protein isoform does not require differential expression of the gene encoding the protein in question. As used herein, the term "Depression-Associated Protein Isoform"

refers to a protein isoform that is differentially present in CSF from a subject having BAD compared with CSF from a subject free from BAD.

Two groups of DPIs have been identified by amino acid sequencing of DFs. DPIs were isolated, subjected to proteolysis, and analyzed by mass spectrometry using the methods and apparatus of the Preferred Technology. One skilled in the art can identify sequence information from proteins analyzed by mass spectrometry and/or tandem mass spectrometry using various spectral interpretation methods and database searching tools. Examples of some of these methods and tools can be found at the Swiss Institute of Bioinformatics web site at http://www.expasy.ch/, and the European Molecular Biology Laboratory web site at www.mann.embl-heidelberg.de/Services/PeptideSearch/. Identification of BPIs was performed primarily using the SEQUEST search program (Eng et al., 1994, J. Am. Soc. Mass Spectrom. 5:976-989) with raw, uninterpreted tandem mass spectra of tryptic digest peptides as described in the Examples, infra. The first group consists of DPIs that are decreased in the CSF of subjects having BAD as compared with the CSF of subjects free from BAD, where the differential presence is significant. The amino acid sequences of tryptic digest peptides of these DPIs identified by tandem mass spectrometry and database searching as described in the Examples, infra are listed in Table IV, in addition to their corresponding pIs and MWs. For DPI- 45 and DPI-213, the partial sequence information for these DPIs derived from tandem mass spectrometry was not found to be described in any known public database. These DPIs are listed as 'NOVEL' in Table IV, and further described below.

Table IV. DPIs Decreased in CSF of Subjects Having BAD

DF#	DPI#	pI	MW (Da)	Amino Acid Sequences of Tryptic Digest Peptides
DF-3	DPI-139	5.71	65446	VWVYPPEK, EWFWDLATGTMK
DF-3	DPI-140	5.71	65446	DVFLGMFLYEYAR, FQNALLVR
DF-4	DPI-2	4.82	155156	LICSELNGR, EGLDLQVLEDSGR, QFPTPGIR, QYDSILR
DF-6	DPI-141	9.05	18350	AQGFTEDTIVFLPQTDK, TMLLQPAGSLGSYSYR, APEAQVSVQPNFQQDK

DF-7	DPI-3	9.07	17183	LVGGPMDASVEEEGVR
DF-8	DPI-4	7.18	20921	AQGFTEDTIVFLPQTDK, TMLLQPAGSLGSYSYR, APEAQVSVQPNFQQDK
DF-9	DPI-103	4.83	184426	SMEQNGPGLEYR, DGNPFYFTDH
DF-10	DPI-5	4.93	27009	ADGSYAAWLSR, DHAVDLIQK, VLSLAQEQVGGSPEK
DF-11	DPI-142	4.89	105482	SSSELNGVSTTSVVK
DF-14	DPI-104	4.55	24374	TMLLQPAGSLGSYSYR
DF-17	DPI-105	5.75	186832	AIGYLNTGYQR, LPPNVVEESAR
DF-18	DPI-6	4.29	62182	DQDGEILLPR, QELEDLER
DF-19	DPI-106	5.66	186832	LPPNVVEESAR
DF-22	DPI-7	4.47	54791	EHAVEGDCDFQLLK, HTLNQIDEVK
DF-23	DPI-143	5.64	58495	WLQGSQELPR
DF-24	DPI-107	4.86	153822	FVVTDGGITR, IIMLFTDGGEER
DF-25	DPI-8	5.67	32549	SELEEQLTPVAEETR, LGPLVEQGR, LEEQAQQIR, LGADMEDVR SWFEPLVEDMQR GEVQAMLGQSTEELR AATVGSLAGQPLQER
DF-25	DPI-108	5.67	32549	AADDTWEPFASGK, GSPAINVAVHVFR
DF-26	DPI-144	3.94	48929	TEDTIFLR, TYMLAFDVNDEK, WFYIASAFR
DF-28	DPI-9	9.59	68368	AEFQDALEK, SCGLHQLLR, LNMGITDLQGLR, LTVAAPPSGGPGFLSIER, VDFTLSSER
DF-29	DPI-10	9.35	13879	LVGGPMDASVEEEGVR
DF-30	DPI-11	5.02	80131	CEGPIPDVTFELLR, HQFLLTGDTQGR
DF-31	DPI-12	5.13	82859	ELLESYIDGR
DF-33	DPI-13	5.12	37524	KYNELLK, EILSVDCSTNNPSQAK, ELDESLQVAER
DF-34	DPI-109	8.14	13783	LVGGPMDASVEEEGVR, ALDFAVGEYNK
DF-35	DPI-145	6.12	17901	ALEESNYELEGK

DF-36	DPI-14	9.04	11790	LVGGPMDASVEEEGVR, ALDFAVGEYNK
DF-37	DPI-15	5.49	57515	LPGIVAEGR
DF-37	DPI-110	5.49	57515	GSPAINVAVHVFR
DF-39	DPI-17	4.37	102603	VESLEQEAANER
DF-39	DPI-18	4.37	102603	LLDSLPSDTR
DF-40	DPI-19	5.04	36196	SELEEQLTPVAEETR, SWFEPLVEDMQR, LGPLVEQGR, GEVQAMLGQSTEELR, LEEQAQQIR
DF-40	DPI-20	5.04	36196	ASSIIDELFQDR, ELDESLQVAER, TLLSNLEEAK
DF-41	DPI-21	4.64	146425	EGLDLQVLEDSGR
DF-41	DPI-111	4.64	146425	TQPVQGEPSAPK
DF-42	DPI-22	4.5	53966	EHAVEGDCDFQLLK, HTLNQIDEVK
DF-43	DPI-23	9.86	34695	FISLGEACK, VFLDCCNYITELR, TGLQEVEVK
DF-43	DPI-24	9.86	34695	TLEAQLTPR
DF-44	DPI-25	4.48	110040	QQLVETHMAR, VESLEQEAANER, AVIQHFQEK
DF-51	DPI-29	5.98	90092	EPGLQIWR, YIETDPANR, HVVPNEVVVQR
DF-52	DPI-30	6.37	101661	ALFVSEEEK, LPPTTTCQQQK, CLVNLIEK, VASYGVKPR, QLNEINYEDHK, LELEDSVTYHCSR, GDSGGPLIVHK
DF-55	DPI-34	5.67	48092	TVQAVLTVPK, SSFVAPLEK, ELLDTVTAPQK, LAAAVSNFGYDLYR, LSYEGEVTK, TSLEDFYLDEER, DTDTGALLFIGK
DF-55	DPI-113	5.67	48092	LCTVATLR
DF-56	DPI-35	5.89	91613	RTPITVVK, EPGLQIWR, HVVPNEVVVQR, EVQGFESATFLGYFK
DF-58	DPI-37	4.77	91613	VEDPESTLFGSVIR, LLEVPEGR

DF-60	DPI-38	6.05	47450	SSFVAPLEK, TSLEDFYLDEER, LAAAVSNFGYDLYR
DF-61	DPI-39	6.93	27331	LVHGGPCDK, YTNWIQK, KPNLQVFLGK, ESSQEQSSVVR GLVSWGNIPCGSK, LSELIQPLPLER, EKPGVYTNVCR
DF-64	DPI-44	4.5	61297	MEEVEAMLLPETLK, EIGELYLPK, NLAVSQVVHK, WEMPFDPQDTHQSR, ITLLSALVETR
DF-65	DPI-45	4.86	60009	NOVEL
DF-65	DPI-146	4.86	60009	DPTFIPAPIQAK, ALQDQLVLVAAK
DF-66	DPI-47	7.10	23117	AQGFTEDTIVFLPQTDK, TMLLQPAGSLGSYSYR, APEAQVSVQPNFQQDK
DF-67	DPI-115	4.94	12681	LVNEVTEFAK
DF-68	DPI-49	9.18	39998	TLLSVGGWNFGSQR, FPLTNAIK, QHFTTLIK, FSNTDYAVGYMLR, GNQWVGYDDQESVK, EGDGSCFPDALDR, LVMGIPTFGR
DF-69	DPI-50	5.90	23795	AQGFTEDTIVFLPQTDK, TMLLQPAGSLGSYSYR, APEAQVSVQPNFQQDK
DF-70	DPI-51	4.91	38741	AGDFLEANYMNLQR, DICEEQVNSLPGSITK, DFDFVPPVVR, GYTQQLAFR
DF-70	DPI-116	4.91	38741	ASSIIDELFQDR, ELDESLQVAER
DF-71	DPI-52	7.09	21231	TMLLQPAGSLGSYSYR
DF-170	DPI-185	9.05	19478	TMLLQPAGSLGSYSYR, AQGFTEDTIVFLPQTDK, APEAQVSVQPNFQQDK
DF-172	DPI-186	4.29	53154	DQDGEILLPR
DF-174	DPI-187	5.59	56791	DPTFIPAPIQAK, SLDFTELDVAAEK
DF-176	DPI-188	4.47	128027	AVIQHFQEK, VESLEQEAANER, QQLVETHMAR, VEAMLNDR

DF-178	DPI-189	8.17	12814	LVGGPMDASVEEEGVR,
DF-179	DPI-190	4.63	33899	ELDESLQVAER
DF-180	DPI-191	5.68	50944	TALASGGVLDASGDYR, EPGEFALLR, NELVQLYQVGEVR, WVNLPEESLLR
DF-188	DPI-192	4.31	63376	DQDGEILLPR, QELEDLER
DF-189	DPI-193	9.05	19032	TMLLQPAGSLGSYSYR, AQGFTEDTIVFLPQTDK
DF-190	DPI-194	4.55	109447	VESLEQEAANER
DF-194	DPI-195	4.57	30225	IPTTFENGR
DF-197	DPI-196	4.40	27223	IPTTFENGR
DF-198	DPI-197	7.89	57515	GDYPLEAVR, LFEELVR, GIFPVLCK, DPVQEAWAEDVDLR,
DF-200	DPI-198	6.34	20539	EVDSGNDIYGNPIK, SDGSCAWYR
DF-201	DPI-199	6.89	31721	VHYTVCIWR, CSVFYGAPSK, GLQDEDGYR, FACYYPR, VEYGFQVK, ITQVLHFTK
DF-202	DPI-200	6.30	23117	LVNEVTEFAK
DF-203	DPI-201	4.70	37742	ASSIIDELFQDR, ELDESLQVAER
DF-204	DPI-202	4.46	32643	IPTTFENGR
DF-207	DPI-203	5.95	13129	HVGDLGNVTADK
DF-208	DPI-204	8.16	24182	APEAQVSVQPNFQQDK, TMLLQPAGSLGSYSYR, AQGFTEDTIVFLPQTDK
DF-210	DPI-205	5.37	123390	AFLFQDTPR, YLELESSGHR, NNAHGYFK, TCPTCNDFHGLVQK, LDQCYCER, HNGQIWVLENDR, CVTDPCQADTIR
DF-211	DPI-206	4.72	20882	THPHFVIPYR
DF-213	DPI-207	5.19	48827	YYTVFDR
DF-213	DPI-208	5.19	48827	YTFELSR
DF-213	DPI-209	5.19	48827	YICENQDSISSK, AAFTECCQAADK
DF-213	DPI-210	5.19	48827	TALASGGVLDASGDYR, YEAAVPDPR, EPGEFALLR
DF-214	DPI-211	4.51	102603	VESLEQEAANER

DF-215	DPI-212	5.04	57690	RVWELSK, VAEGTQVLELPFK, LPGIVAEGR, DDLYVSDAFHK, EVPLNTIIFMGR
DF-215	DPI-213	5.04	57690	NOVEL
DF-216	DPI-214	5.03	39080	ASSIIDELFQDR
DF-217	DPI-215	4.53	36239	ELDESLQVAER
DF-218	DPI-216	4.74	30882	IPTTFENGR
DF-220	DPI-217	4.31	47931	HTLNQIDEVK
DF-222	DPI-218	4.69	156503	QPEYAVVQR
DF-224	DPI-219	6.10	184426	AIGYLNTGYQR, LPPNVVEESAR
DF-225	DPI-220	4.41	24762	LPYTASSGLMAPR
DF-226	DPI-221	5.08	26332	TMLLQPAGSLGSYSYR, AQGFTEDTIVFLPQTDK
DF-227	DPI-222	6.06	184426	AIGYLNTGYQR, LPPNVVEESAR

The second group consists of DPIs that are increased in the CSF of subjects having BAD as compared with the CSF of subjects free from BAD, where the differential presence is significant. The amino acid sequences of tryptic digest peptides of these DPIs identified by tandem mass spectrometry and database searching as described in the Examples, infra are listed in Table V, in addition to their corresponding pIs and MWs.

Table V. DPIs Increased In CSF of Subjects Having BAD

DF#	DPI#	pI	MW (Da)	Amino Acid Sequences of Tryptic Digest Peptides
DF-76	DPI-57	7.24	11749	VVAGVANALAHK, GTFATLSELHCDK, LLVVYPWTQR
DF-77	DPI-58	7.09	27075	GGPFSDSYR, ESISVSSEQLAQFR
DF-78	DPI-147	9.01	10999	VVIGMDVAASEFFR
DF-82	DPI-151	6.61	11467	EFTPPVQAAYQK, LLVVYPWTQR, VNVDAVGGEALGR
DF-82	DPI-152	6.61	11467	QMLNIPNQPK
DF-84	DPI-154	7.98	11312	MFLSFPTTK, FLASVSTVLTSK
DF-84	DPI-155	7.98	11312	LVGGPMDASVEEEGVR,

				QIVAGVNYFLDVELGR, ASNDMYHSR
DF-86	DPI-59	4.86	28850	IPTTFENGR
DF-87	DPI-60	6.92	11749	TDAENEFVTLK
DF-94	DPI-65	7.48	11668	LVGGPMDASVEEEGVR
DF-94	DPI-119	7.48	11668	VHLTPEEK, , VVAGVANALAHK, GTFATLSELHCDK, LLVVYPWTQR
DF-95	DPI-159	7.05	11388	VHLTPEEK, NVDEVGGEALGR, LLVVYPWTQR, EFTPPVQAAYQK, VLGAFSDGLAHLDNLK
DF-96	DPI-66	7.48	11932	ALDFAVGEYNK, LVGGPMDASVEEEGVR
DF-97	DPI-160	6.65	11872	LLVVYPWTQR, EFTPPVQAAYQK
DF-97	DPI-161	6.65	11872	ALDFAVGEYNK
DF-100	DPI-162	7.01	57356	LFAYPDTHR, LNVITVGPR, LSQEDPDYGIR
DF-101	DPI-67	6.8	32080	VVEEQESR, VEYGFQVK, ITQVLHFTK, GLQDEDGYR, FACYYPR, VHYTVCIWR, CSVFYGAPSK,
DF-102	DPI-163	7.31	11037	MFLSFPTTK, VHLTPEEK, EFTPPVQAAYQK, IGGHAGEYGAEALER, LLVVYPWTQR, VLGAFSDGLAHLDNLK
DF-102	DPI-164	7.31	11037	LLVVFFLEHR
DF-102	DPI-165	7.31	11037	ILVTAEGISFLK
DF-102	DPI-166	7.31	11037	LLSSSAEETWR
DF-103	DPI-69	5.5	20607	QITVNDLPVGR
DF-104	DPI-167	4.64	10735	GCSFLPDPYQK
DF-104	DPI-168	4.64	10735	VDTVDPPYPR
DF-104	DPI-169	4.64	10735	AQGFTEDTIVFLPQTDK
DF-105	DPI-170	6.62	39221	YDTVHGQWK, DAPMFVVGVNEDK, VPTVDVSVVDLTVR, AGIALNDHFIK
DF-106	DPI-120	4.59	40613	IPTTFENGR
DF-106	DPI-121	4.59	40613	NVLVTLYER
DF-107	DPI-171	5.88	10560	LLVVYPWTQR

DF-108	DPI-172	6	11753	EFTPPVQAAYQK, LLVVYPWTQR, VHLTPEEK
DF-110	DPI-173	6.39	12122	EFTPPVQAAYQK, VVAGVANALAHK, VHLTPEEK, LLVVYPWTQR
DF-112	DPI-174	7.42	43773	FEEILTR, SFLVWVNEEDHLR
DF-115	DPI-71	5.59	39882	IRPFFPQQ, LESDVSAQMEYCR, DNDGWLTSDPR, DNENVVNEYSSELEK
DF-118	DPI-175	7.81	43773	EPGLQIWR, EVQGFESATFLGYFK, HVVPNEVVVQR, QTQVSVLPEGGETPLFK
DF-120	DPI-123	7.01	40510	LNDLEEALQQAK
DF-123	DPI-72	5.19	12080	GSPAINVAVHVFR
DF-124	DPI-176	5.54	21908	PPYTVVYFPVR
DF-125	DPI-73	6.18	43043	CCTESLVNR, VPQVSTPTLVEVAR, IYEATLEDCCAK
DF-127	DPI-177	7.85	45269	QTQVSVLPEGGETPLFK
DF-130	DPI-178	7.27	48975	VVIGMDVAASEFFR
DF-131	DPI-76	5.79	39536	IRPFFPQQ, DNDGWLTSDPR, QDGSVDFGR, LESDVSAQMEYCR, EDGGGWWYNR
DF-134	DPI-78	6.39	44664	SIPQVSPVR, IVQLIQDTR
DF-134	DPI-124	6.39	44664	LVAEFDFR
DF-135	DPI-79	5.3	43920	SYELPDGQVITIGNER, AGFAGDDAPR, GYSFTTTAER, QEYDESGPSIVHR
DF-137	DPI-179	6.66	19935	ALEESNYELEGK
DF-138	DPI-87	5.01	43626	LEPYADQLR, LTPYADEFK, LAPLAEDVR, ISASAEELR
DF-142	DPI-181	5.1	46974	YYCFQGNQFLR
DF-144	DPI-127	4.62	28747	ASSIIDELFQDR
DF-144	DPI-128	4.62	28747	NPNLPPETVDSLK, NILTSNNIDVK, IPTTFENGR
DF-144	DPI-129	4.62	28747	GECQAEGVLFFQGDR
DF-145	DPI-88	6.53	10226	SCDLALLETYCATPAK, GIVEECCFR
DF-146	DPI-89	5.03	46659	QGSFQGGFR, AEMADQAAAWLTR, VLSLAQEQVGGSPEK

DF-148	DPI-90	6.29	80131	VSVFVPPR
DF-153	DPI-92	4.95	44515	IDQTVEELR, LEPYADQLR, ALVQQMEQLR, TQVNTQAEQLR
DF-155	DPI-93	7.03	155828	GPPGPPGGVVVR, VEVLAGDLR, GGEILIPCQPR, FAQLNLAAEDTR
DF-158	DPI-184	7.7	40407	GNQWVGYDDQESVK, LVMGIPTFGR, FSNTDYAVGYMLR, ILGQQVPYATK
DF-161	DPI-96	6.88	40613	HIYLLPSGR, VNLGVGAYR, NFGLYNER, ITWSNPPAQGAR, VGGVQSLGGTGALR
DF-164	DPI-135	4.96	74524	NGVAQEPVHLDSPAIK, HQFLLTGDTQGR, ATWSGAVLAGR
DF-231	DPI-223	7.02	33025	CSVFYGAPSK, FACYYPR, VEYGFQVK, ITQVLHFTK
DF-235	DPI-224	9.75	11627	LVGGPMDASVEEEGVR
DF-236	DPI-225	7.05	32024	CSVFYGAPSK, GLQDEDGYR, FACYYPR, VEYGFQVK, ITQVLHFTK
DF-237	DPI-226	6.69	39193	INHGILYDEEK, EIMENYNIALR
DF-239	DPI-227	5.73	22738	TMLLQPAGSLGSYSYR, AQGFTEDTIVFLPQTDK
DF-239	DPI-228	5.73	22738	LVNEVTEFAK, YLYEIAR
DF-240	DPI-229	4.86	148596	EGLDLQVLEDSGR
DF-261	DPI-230	4.17	40285	WFYIASAFR, TEDTIFLR, YVGGQEHFAHLLILR, TYMLAFDVNDEK, NWGLSVYADKPETTK, EQLGEFYEALDCLR
DF-262	DPI-231	7.44	26066	LLIYWASTR, SGTASVVCLLNNFYPR
DF-262	DPI-232	7.44	26066	GGPLDGTYR, SADFTNFDPR
DF-265	DPI-233	7.81	24686	TMLLQPAGSLGSYSYR, AQGFTEDTIVFLPQTDK
DF-266	DPI-234	6.45	20882	LVMGIPTFGR
DF-269	DPI-235	5	31104	GSPAINVAVHVFR, AADDTWEPFASGK
DF-271	DPI-236	9.58	21021	TMLLQPAGSLGSYSYR
DF-273	DPI-237	5.6	12917	GSPAINVAVHVFR, AADDTWEPFASGK

DF-275	DPI-238	6.23	12206	FEETTADGR
DF-281	DPI-239	6.48	31008	DVVLTTTFVDDIKALPTTYEK, AIEDYINEFSVR, CLCACPFKFEGIACEISK
DF-282	DPI-240	5.98	45728	YICENQDSISSK, AAFTECCQAADK, DVFLGMFLYEYAR
DF-283	DPI-241	9.24	11400	LVGGPMDASVEEEGVR, ALDFAVGEYNK, QIVAGVNYFLDVELGR
DF-286	DPI-242	6.11	12038	LGVEFDETTADDR,
DF-287	DPI-243	9.59	22365	TMLLQPAGSLGSYSYR, AQGFTEDTIVFLPQTDK
DF-288	DPI-244	5	29267	AATVGSLAGQPLQER
DF-289	DPI-245	5.58	32266	AATVGSLAGQPLQER
DF-289	DPI-246	5.58	32266	EILSVDCSTNNPSQAK
DF-289	DPI-247	5.58	32266	GSPAINVAVHVFR, AADDTWEPFASGK
DF-291	DPI-248	8.79	23405	TMLLQPAGSLGSYSYR, AQGFTEDTIVFLPQTDK
DF-295	DPI-249	8.54	54625	TIYTPGSTVLYR, IPIEDGSGEVVLSR
DF-297	DPI-250	5.49	15277	SELEEQLTPVAEETR
DF-299	DPI-251	7.15	15381	EPGLQIWR, HVVPNEVVVQR
DF-300	DPI-252	4.94	16019	AATVGSLAGQPLQER, LEEQAQQIR
DF-302	DPI-253	7.28	34494	TELLPGDR,DNLAIQTR
DF-303	DPI-254	7.48	59646	EMSGSPASGIPVK, LNMGITDLQGLR, GQIVFMNR
DF-306	DPI-255	6.36	24567	DFTPVCTTELGR, LPFPIIDDR, LSILYPATTGR
DF-310	DPI-256	5.53	142313	LPPNVVEESAR
DF-311	DPI-257	6.16	35402	TMLLQPAGSLGSYSYR
DF-313	DPI-258	5.5	80131	GLCVATPVQLR, EELVYELNPLDHR, QGSFQGGFR
DF-316	DPI-259	5.43	43086	LPGIVAEGR
DF-322	DPI-260	8.79	22458	TMLLQPAGSLGSYSYR
DF-323	DPI-261	6.57	21549	QSLEASLAETEGR
DF-326	DPI-262	5.82	41902	TEDTIFLR
DF-326	DPI-263	5.82	41902	VNEPSILEMSR
DF-327	DPI-264	5.22	13359	GSPAINVAVHVFR, AADDTWEPFASGK

DF-329	DPI-265	4.19	20607	FSSCGGGGGSFGAGGGFGSR
DF-330	DPI-266	5.54	37852	AREDIFMETLK, DYIEFNK, WEAEPVYVQR, AYLEEECPATLR, IDVHWTR, AGEVQEPELR
DF-332	DPI-267	6.34	53167	DFYVDENTTVR
DF-334	DPI-268	4.44	37962	FISLGEACK, TGLQEVEVK
DF-335	DPI-269	4.83	55426	SGNENGEFYLR, ADQVCINLR
DF-342	DPI-270	5.12	15174	SELEEQLTPVAEETR, GEVQAMLGQSTEELR
DF-343	DPI-271	5.42	18290	QSLEASLAETEGR
DF-343	DPI-272	5.42	18290	LEGEACGVYTPR
DF-347	DPI-273	4.93	25356	TMLLQPAGSLGSYSYR, AQGFTEDTIVFLPQTDK
DF-349	DPI-274	5.84	65031	NFPSPVDAAFR, VWVYPPEK, GECQAEGVLFFQGDR, DYFMPCPGR, RLWWLDLK
DF-351	DPI-275	9.07	23405	TMLLQPAGSLGSYSYR, AQGFTEDTIVFLPQTDK
DF-353	DPI-276	5.36	28921	LASNISPR
DF-355	DPI-277	6.18	187641	LPPNVVEESAR
DF-356	DPI-278	4.93	102603	TGYYFDGISR, MCVDVNECQR, CLAFECPENYR
DF-357	DPI-279	7.02	70955	HSTVLENLPDK, DQYELLCR, SPDFQLFSSSHGK, CGLVPVLAENYK, SSGPDLNWNNLK, FDQFFGEGCAPGSQR, EPVDNAENCHLAR
DF-357	DPI-280	7.02	70955	IPIEDGSGEVVLSR
DF-358	DPI-281	4.95	45574	QGSFQGGFR, TEQWSTLPPETK, DHAVDLIQK, ADGSYAAWLSR, VLSLAQEQVGGSPEK, AEMADQASAWLTR

As will be evident to one of skill in the art, based upon the present description, a given DPI can be described according to the data provided for that DPI in Table IV or V. The DPI is a protein comprising a peptide sequence described for that DPI (preferably comprising a plurality of, more preferably all of, the peptide sequences

described for that DPI) and has a pI of about the value stated for that DPI (preferably within about 10%, more preferably within about 5% still more preferably within about 1% of the stated value) and has a MW of about the value stated for that DPI (preferably within about 10%, more preferably within about 5%, still more preferably within about 1% of the stated value). Proteins comprising the peptide sequences provided in Table IV and V can be identified by searching sequence databases with those peptides using search tools known to those skilled in the art. Examples of search algorithm tools that can be used to identify proteins from peptide sequences include:

- BLAST (Basic Local Alignment Search Tool) ; BLAST is maintained at the National Center for Biotechnology Information (NCBI) (http://www.ncbi.nlm.nih.gov) and is based on a statistical theory developed by Samuel Karlin and Steven Altschul (*Proc. Natl Acad. Sci.* USA (1990) 87:2284-2268), later modified as in Karlin and Altschul (*Proc. Natl Acad. Sci.* (1993) 90:5873). BLASTP can be used to search a protein sequence against a protein database. TBLASTN can be used to search a Protein Sequence against a Nucleotide Database, by translating each database Nucleotide sequence in all 6 reading frames.
- FASTA as described in Pearson and Lipman (1988) *Proc. Natl. Acad. Sci.* 85:2444-8. See also Pearson *Methods Enzymol.* (1990) 183:63-98 and Pearson *Genomics* (1991) 11(3):635-50.

Examples of available protein sequence databases include:

- The nr protein database maintained at the National Center for Biotechnology Information (NCBI) (http://www.ncbi.nlm.nih.gov). The nr protein database is compiled of entries from various sources including SwissProt, SwissProt updates, PIR, and PDB. The BLAST resource is available for sequence searching.
- SwissProt and TrEMBL databases developed by the Swiss Bioinformatics Institute (SIB) and the European can be found at http://www.expasy.ch. BLASTP resources are available for sequence searching.
- The PIR-International Protein Sequence Database maintained by the Protein Information Resource (PIR), in collaboration with the Munich Information Center for Protein Sequences (MIPS) and the Japanese International Protein Sequence Database (JIPID). The Protein Identification Resource (PIR) is a division of the National Biomedical Research Foundation (NBRF) which is affiliated with Georgetown University Medical Center and can be found at http://www

nbrf.georgetown.edu/pir/searchdb.html. The database can be searched using BLAST and FASTA search algorithm tools.

- The Protein Data Bank, maintained by Brookhaven National Laboratory (Long Island, New York, USA) which can be found at http://www.rcsb.org/pdb/. The FASTA resource is available at this website for sequence searching.

In one embodiment, CSF from a subject is analyzed for quantitative detection of one or more of the following DPIs: DPI-2, DPI-3, DPI-4, DPI-5, DPI-6, DPI-7, DPI-8, DPI-9, DPI-10, DPI-11, DPI-12, DPI-13, DPI-14, DPI-15, DPI-17, DPI-18, DPI-19, DPI-20, DPI-21, DPI-22, DPI-23, DPI-24, DPI-25, DPI-29, DPI-30, DPI-34, DPI-35, DPI-37, DPI-38, DPI-39, DPI-44, DPI-45, DPI-47, DPI-49, DPI-50, DPI-51, DPI-52, DPI-103, DPI-104, DPI-105, DPI-106, DPI-107, DPI-108, DPI-109, DPI-110, DPI-111, DPI-113, DPI-115, DPI-116, DPI-139, DPI-140, DPI-141, DPI-142, DPI-143, DPI-144, DPI-145, DPI-146, DPI-185, DPI-186, DPI-187, DPI-188, DPI-189, DPI-190, DPI-191, DPI-192, DPI-193, DPI-194, DPI-195, DPI-196, DPI-197, DPI-198, DPI-199, DPI-200, DPI-201, DPI-202, DPI-203, DPI-204, DPI-205, DPI-206, DPI-207, DPI-208, DPI-209, DPI-210, DPI-211, DPI-212, DPI-213, DPI-214, DPI-215, DPI-216, DPI-217, DPI-218, DPI-219, DPI-220, DPI-221, DPI-222, or any combination of them, wherein a decreased abundance of the DPI or DPIs (or any combination of them) in the CSF from the subject relative to CSF from a subject or subjects free from BAD (e.g., a control sample or a previously determined reference range) indicates the presence of BAD.

In another embodiment of the invention, CSF from a subject is analyzed for quantitative detection of one or more of the following DPIs: DPI-57, DPI-58, DPI-59, DPI-60, DPI-65, DPI-66, DPI-67, DPI-69, DPI-71, DPI-72, DPI-73, DPI-76, DPI-78, DPI-79, DPI-87, DPI-88, DPI-89, DPI-90, DPI-92, DPI-93, DPI-96, DPI-119, DPI-120, DPI-121, DPI-123, DPI-124, DPI-127, DPI-128, DPI-129, DPI-135, DPI-147, DPI-151, DPI-152, DPI-154, DPI-155, DPI-159, DPI-160, DPI-161, DPI-162, DPI-163, DPI-164, DPI-165, DPI-166, DPI-167, DPI-168, DPI-169, DPI-170, DPI-171, DPI-172, DPI-173, DPI-174, DPI-175, DPI-176, DPI-177, DPI-178, DPI-179, DPI-181, DPI-184, DPI-223, DPI-224, DPI-225, DPI-226, DPI-227, DPI-228, DPI-229, DPI-230, DPI-231, DPI-232, DPI-233, DPI-234, DPI-235, DPI-236, DPI-237, DPI-238, DPI-239, DPI-240, DPI-241, DPI-242, DPI-243, DPI-244, DPI-245, DPI-246, DPI-247, DPI-248, DPI-249, DPI-250, DPI-251, DPI-252, DPI-253, DPI-254, DPI-

255, DPI-256, DPI-257, DPI-258, DPI-259, DPI-260, DPI-261, DPI-262, DPI-263; DPI-264, DPI-265, DPI-266, DPI-267, DPI-268, DPI-269, DPI-270, DPI-271, DPI-272, DPI-273, DPI-274, DPI-275, DPI-276, DPI-277, DPI-278, DPI-279, DPI-280, DPI-281, or any combination of them, wherein an increased abundance of the DPI or DPIs (or any combination of them) in CSF from the subject relative to CSF from a subject or subjects free from BAD (e.g., a control sample or a previously determined reference range) indicates the presence of BAD.

In a further embodiment, CSF from a subject is analyzed for quantitative detection of (a) one or more DPIs, or any combination of them, whose decreased abundance indicates the presence of BAD, i.e., DPI-2, DPI-3, DPI-4, DPI-5, DPI-6, DPI-7, DPI-8, DPI-9, DPI-10, DPI-11, DPI-12, DPI-13, DPI-14, DPI-15, DPI-17, DPI-18, DPI-19, DPI-20, DPI-21, DPI-22, DPI-23, DPI-24, DPI-25, DPI-29, DPI-30, DPI-34, DPI-35, DPI-37, DPI-38, DPI-39, DPI-44, DPI-45, DPI-47, DPI-49, DPI-50, DPI-51, DPI-52, DPI-103, DPI-104, DPI-105, DPI-106, DPI-107, DPI-108, DPI-109, DPI-110, DPI-111, DPI-113, DPI-115, DPI-116, DPI-139, DPI-140, DPI-141, DPI-142, DPI-143, DPI-144, DPI-145, DPI-146, DPI-185, DPI-186, DPI-187, DPI-188, DPI-189, DPI-190, DPI-191, DPI-192, DPI-193, DPI-194, DPI-195, DPI-196, DPI-197, DPI-198, DPI-199, DPI-200, DPI-201, DPI-202, DPI-203, DPI-204, DPI-205, DPI-206, DPI-207, DPI-208, DPI-209, DPI-210, DPI-211, DPI-212, DPI-213, DPI-214, DPI-215, DPI-216, DPI-217, DPI-218, DPI-219, DPI-220, DPI-221, DPI-222; and (b) one or more DPIs, or any combination of them, whose increased abundance indicates the presence of BAD, i.e., DPI-57, DPI-58, DPI-59, DPI-60, DPI-65, DPI-66, DPI-67, DPI-69, DPI-71, DPI-72, DPI-73, DPI-76, DPI-78, DPI-79, DPI-87, DPI-88, DPI-89, DPI-90, DPI-92, DPI-93, DPI-96, DPI-119, DPI-120, DPI-121, DPI-123, DPI-124, DPI-127, DPI-128, DPI-129, DPI-135, DPI-147, DPI-151, DPI-152, DPI-154, DPI-155, DPI-159, DPI-160, DPI-161, DPI-162, DPI-163, DPI-164, DPI-165, DPI-166, DPI-167, DPI-168, DPI-169, DPI-170, DPI-171, DPI-172, DPI-173, DPI-174, DPI-175, DPI-176, DPI-177, DPI-178, DPI-179, DPI-181, DPI-184, DPI-223, DPI-224, DPI-225, DPI-226, DPI-227, DPI-228, DPI-229, DPI-230, DPI-231, DPI-232, DPI-233, DPI-234, DPI-235, DPI-236, DPI-237, DPI-238, DPI-239, DPI-240, DPI-241, DPI-242, DPI-243, DPI-244, DPI-245, DPI-246, DPI-247, DPI-248, DPI-249, DPI-250, DPI-251, DPI-252, DPI-253, DPI-254, DPI-255, DPI-256, DPI-257, DPI-258, DPI-259, DPI-260, DPI-261, DPI-262, DPI-263, DPI-264, DPI-265, DPI-

266, DPI-267, DPI-268, DPI-269, DPI-270, DPI-271, DPI-272, DPI-273, DPI-274, DPI-275, DPI-276, DPI-277, DPI-278, DPI-279, DPI-280, DPI-281.

In yet a further embodiment, CSF from a subject is analyzed for quantitative detection of one or more DPIs and one or more previously known biomarkers of BAD (e.g., candidate markers such as hypersensitive platelet glutamate receptors (Berk et al. Int Clin Psychopharmacol 1999 14, 119-22)). In accordance with this embodiment, the abundance of each DPI and known biomarker relative to a control or reference range indicates whether a subject has BAD.

Preferably, the abundance of a DPI is normalized to an Expression Reference Protein Isoform (ERPI). ERPIs can be identified by partial amino acid sequencing of ERFs, which are described above, using the methods and apparatus of the Preferred Technology. The partial amino acid sequences of an ERPI, and the known proteins to which it is homologous is presented in Table VI.

Table IV.

ERPI-#	ERF-#	Amino Acid Sequences of Tryptic Digest Peptides
ERPI-1	ERF-1	EELVYELNPLDHR
ERPI-2	ERF-2	NGVAQEPVHLDSPAIK ATWSGAVLAGR HQFLLTGDTQGR

As shown above, the DPIs described herein include previously unknown proteins, as well as isoforms of known proteins where the isoforms were not previously known to be associated with BAD. For each DPI, the present invention additionally provides: (a) a preparation comprising the isolated DPI; (b) a preparation comprising one or more fragments of the DPI; and (c) antibodies that bind to said DPI, to said fragments, or both to said DPI and to said fragments. As used herein, a DPI is "isolated" when it is present in a preparation that is substantially free of contaminating proteins, i.e., a preparation in which less than 10% (preferably less than 5%, more preferably less than 1%) of the total protein present is contaminating protein(s). A contaminating protein is a protein or protein isoform having a significantly different pI or MW from those of the isolated DPI, as determined by 2D electrophoresis. As used herein, a "significantly different" pI or MW is one that

permits the contaminating protein to be resolved from the DPI on 2D electrophoresis, performed according to the Reference Protocol.

In one embodiment, an isolated protein is provided, said protein comprising a peptide with the amino acid sequence identified in Table IV or V for a DPI, said protein having a pI and MW within 10% (preferably within 5%, more preferably within 1%) of the values identified in Table IV or V for that DPI.

The DPIs of the invention can be qualitatively or quantitatively detected by any method known to those skilled in the art, including but not limited to the Preferred Technology described herein, kinase assays, enzyme assays, binding assays and other functional assays, immunoassays, and western blotting. In one embodiment, the DPIs are separated on a 2-D gel by virtue of their MWs and pIs and visualized by staining the gel. In one embodiment, the DPIs are stained with a fluorescent dye and imaged with a fluorescence scanner. Sypro Red (Molecular Probes, Inc., Eugene, Oregon) is a suitable dye for this purpose. A preferred fluorescent dye is Pyridinium, 4-[2-[4- (dipentylamino)-2-trifluoromethylphenyl] ethenyl]-1-(sulfobutyl)-, inner salt. See U.S. Application No. 09/412,168, filed on October 5, 1999, which is incorporated herein by reference in its entirety.

Alternatively, DPIs can be detected in an immunoassay. In one embodiment, an immunoassay is performed by contacting a sample from a subject to be tested with an anti-DPI antibody under conditions such that immunospecific binding can occur if the DPI is present, and detecting or measuring the amount of any immunospecific binding by the antibody. Anti-DPI antibodies can be produced by the methods and techniques taught herein; examples of such antibodies known in the art are set forth in Table VII. These antibodies shown in Table VII are already known to bind to the protein of which the DPI is itself a family member. Preferably, the anti-DPI antibody preferentially binds to the DPI rather than to other isoforms of the same protein. In a preferred embodiment, the anti-DPI antibody binds to the DPI with at least 2-fold greater affinity, more preferably at least 5-fold greater affinity, still more preferably at least 10-fold greater affinity, than to said other isoforms of the same protein.

DPIs can be transferred from the gel to a suitable membrane (e.g. a PVDF membrane) and subsequently probed in suitable assays that include, without limitation, competitive and non-competitive assay systems using techniques such as western blots and "sandwich" immunoassays using anti-DPI antibodies as described herein, e.g., the antibodies identified in Table VII, or others raised against the DPIs of

interest. The immunoblots can be used to identify those anti-DPI antibodies displaying the selectivity required to immuno-specifically differentiate a DPI from other isoforms encoded by the same gene.

Table VII. Known Antibodies That Recognize DPIs or DPI-Related Polypeptides

DPI#	Antibody	Manufacturer	Catalogue No.
DPI-3	Cystatin C, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	AXL- 574
DPI-5	C4 Complement, Chicken anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-032-02
DPI-8	Apolipoprotein E, LDL, VLDL, Clone: 3D12, Mab anti-Human, frozen/paraffin	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	YM- 5029
DPI-9	C4 Complement, Chicken anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-032-02
DPI-10	Cystatin C, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	AXL- 574
DPI-11	Alpha-1-Acid Glycoprotein, Clone: AGP-47, Mab anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	BYA- 6189-1
DPI-12	Prothrombin, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	AXL- 448/2
DPI-13	Goat anti-Clusterin (human)	RDI RESEARCH DIAGNOSTICS, INC	RDI-CLUSTRCabG
DPI-14	Cystatin C, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	AXL- 574
DPI-15	Antithrombin III, Clone: BL-ATIII/3, Mab anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	BYA- 9009-1
DPI-17	Anti-Alzheimer precursor protein A4	RDI RESEARCH DIAGNOSTICS, INC	RDI-ALZHPA4abm
DPI-19	Apolipoprotein E, LDL, VLDL, Clone: 3D12, Mab anti-Human, frozen/paraffin	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	YM- 5029
DPI-20	Goat anti-Clusterin (human)	RDI RESEARCH DIAGNOSTICS, INC	RDI-CLUSTRCabG
DPI-23	C3 Complement, Chicken anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-001-02
DPI-24	Heparin Cofactor II, Rabbit anti-Human, precipitating	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	YN- RHHCFII
DPI-25	Anti-Alzheimer precursor protein A4	RDI RESEARCH DIAGNOSTICS, INC	RDI-ALZHPA4abm
DPI-29	Gelsolin, plasma + cytoplasmic, Sheep anti-	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	YBG- 4628-6210
DPI-30	Complement Factor B, C3 proactivator, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	AXL- 466/2

DPI-35	Gelsolin, plasma + cytoplasmic, Sheep anti-	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	YBG- 4628-6210
DPI-37	C1r Complement, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	YSRT- AHC002
DPI-44	Alpha-1-Antichymotrypsin, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	AXL- 145/2
DPI-51	C3 Complement, Chicken anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-001-02
DPI-57	Hemoglobin Epsilon Chain, Embryonic, Clone: E1276, Mab anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IRX- E1276
DPI-58	Carbonic Anhydrase I, Human Erythrocytes	BIODESIGN INTERNATIONAL	K59115G
DPI-59	Apolipoprotein D, Clone: 36C6, Mab anti-Human, paraffin, IH/WB	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	MED- CLA457
DPI-60	Mab to Cytokeratin 6	RDI RESEARCH DIAGNOSTICS, INC	RDI-PRO65190
DPI-65	Cystatin C, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	AXL- 574
DPI-66	Cystatin C, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	AXL- 574
DPI-67	C4 Complement, Chicken anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-032-02
DPI-71	Fibrinogen, Fibrin I, B-beta chain (Bßß 1-42), Clone: 18C6, Mab anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	NYB- 18C6
DPI-72	Transthyretin, Prealbuminm, 55kD, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	MED- CLA 193
DPI-73	Albumin, Human, Chicken anti-	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-026-02
DPI-75	Rabbit anti-14-3-3B (Broadly Reactive)	RDI RESEARCH DIAGNOSTICS, INC	RDI-1433BNabr
DPI-76	Fibrinogen, Fibrin I, B-beta chain (Bßß 1-42), Clone: 18C6, Mab anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	NYB- 18C6
DPI-79	Actin, beta, Clone: AC-74, Mab anti-	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	BYA- 6553-1
DPI-87	Apolipoprotein A (HDL), Sheep anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	ACL- 20075AP
DPI-88	Insulin Like Growth Factor II (IGF-II), Clone: W2H1, Mab anti-, frozen, IH/ELISA/RIA	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	MAS- 976p
DPI-89	C4 Complement, Chicken anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-032-02
DPI-90	Gel	DAKO - 1998 CATALOGUE	A0475
DPI-92	Apolipoprotein A (HDL),	ACCURATE CHEMICAL &	ACL- 20075AP

	Sheep anti-Human	SCIENTIFIC CORPORATION	
DPI-108	Transthyretin, Prealbuminm, 55kD, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	MED- CLA 193
DPI-109	Cystatin C, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	AXL- 574
DPI-110	Transthyretin, Prealbuminm, 55kD, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	MED- CLA 193
DPI-113	Albumin, Human, Chicken anti-	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-026-02
DPI-115	Albumin, Human, Chicken anti-	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-026-02
DPI-116	Goat anti-Clusterin (human)	RDI RESEARCH DIAGNOSTICS, INC	RDI-CLUSTRCabG
DPI-119	Hemoglobin, Goat anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	
DPI-120	Apolipoprotein D, Clone: 36C6, Mab anti-Human, paraffin, IH/WB	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	MED- CLA457
DPI-127	Goat anti-Clusterin (human)	RDI RESEARCH DIAGNOSTICS, INC	RDI-CLUSTRCabG
DPI-128	Apolipoprotein D, Clone: 36C6, Mab anti-Human, paraffin, IH/WB	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	MED- CLA457
DPI-129	Hemopexin, Beta-1, Rabbit anti-Human, precipitating	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	YN- RHHPX
DPI-135	Alpha-1-Acid Glycoprotein, Clone: AGP-47, Mab anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	BYA- 6189-1
DPI-139	Hemopexin, Beta-1, Rabbit anti-Human, precipitating	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	YN- RHHPX
DPI-140	Albumin, Human, Chicken anti-	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-026-02
DPI-143	Monoclonal mouse anti-human IgA1	RDI RESEARCH DIAGNOSTICS, INC	RDI-TRK1A2-2B5
DPI-144	Alpha-1-Acid Glycoprotein, Clone: AGP-47, Mab anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	BYA- 6189-1
DPI-145	ANTI-CYTOKERATIN TYPE 10	RDI RESEARCH DIAGNOSTICS, INC	RDI-CBL196
DPI-146	AT1 (306)	SANTA CRUZ BIOTECHNOLOGY, INC - RESEARCH ANTIBODIES 98/99	sc-579
DPI-147	Monoclonal anti-Neuron Specific Enolase	BIODESIGN INTERNATIONAL	M37403M
DPI-155	Cystatin C, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	AXL- 574

DPI-160	Hemoglobin, Goat anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	BMD- J16
DPI-161	Cystatin C, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	AXL- 574
DPI-175	Gelsolin, plasma + cytoplasmic, Sheep anti-	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	YBG- 4628-6210
DPI-177	Gelsolin, plasma + cytoplasmic, Sheep anti-	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	YBG- 4628-6210
DPI-178	Monoclonal anti-Neuron Specific Enolase	BIODESIGN INTERNATIONAL	M37403M
DPI-179	ANTI-CYTOKERATIN TYPE 10	RDI RESEARCH DIAGNOSTICS, INC	RDI-CBL196
DPI-181	Hemopexin, Beta-1, Rabbit anti-Human, precipitating	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	YN- RHHPX
DPI-185	AT1 (306)	SANTA CRUZ BIOTECHNOLOGY, INC - RESEARCH ANTIBODIES 98/99	sc-579
DPI-187	AT1 (306)	SANTA CRUZ BIOTECHNOLOGY, INC - RESEARCH ANTIBODIES 98/99	sc-579
DPI-188	Anti-Alzheimer precursor protein A4	RDI RESEARCH DIAGNOSTICS, INC	RDI-ALZHPA4abm
DPI-189	Cystatin C, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	AXL- 574
DPI-190	Goat anti-Clusterin (human)	RDI RESEARCH DIAGNOSTICS, INC	RDI-CLUSTRCabG
DPI-194	Anti-Alzheimer precursor protein A4	RDI RESEARCH DIAGNOSTICS, INC	RDI-ALZHPA4abm
DPI-195	Apolipoprotein D, Clone: 36C6, Mab anti-Human, paraffin, IH/WB	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	MED- CLA457
DPI-196	Apolipoprotein D, Clone: 36C6, Mab anti-Human, paraffin, IH/WB	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	MED- CLA457
DPI-198	Tissue Inhibitor of Matrix Metalloproteinase 2 (TIMP2) (NO X w/TIMP1), Clone: 3A4, Mab anti-Human, paraffin, IH	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	MED- CLA498
DPI-199	C4 Complement, Chicken anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-032-02
DPI-200	Albumin, Human, Chicken anti-	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-026-02
DPI-201	Goat anti-Clusterin (human)	RDI RESEARCH DIAGNOSTICS, INC	RDI-CLUSTRCabG
DPI-202	Apolipoprotein D, Clone: 36C6, Mab anti-Human, paraffin, IH/WB	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	MED- CLA457

DPI-206	Anti-Aizheimer precursor protein A4	RDI RESEARCH DIAGNOSTICS, INC	RDI-ALZHPA4abm
DPI-209	Albumin, Human, Chicken anti-	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-026-02
DPI-211	Anti-Alzheimer precursor protein A4	RDI RESEARCH DIAGNOSTICS, INC	RDI-ALZHPA4abm
DPI-212	Antithrombin III, Clone: BL-ATIII/3, Mab anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	BYA- 9009-1
DPI-214	Goat anti-Clusterin (human)	RDI RESEARCH DIAGNOSTICS, INC	RDI-CLUSTRCabG
DPI-215	Goat anti-Clusterin (human)	RDI RESEARCH DIAGNOSTICS, INC	RDI-CLUSTRCabG
DPI-216	Apolipoprotein D, Clone: 36C6, Mab anti-Human, paraffin, IH/WB	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	MED- CLA457
DPI-223	C4 Complement, Chicken anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-032-02
DPI-224	Cystatin C, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	AXL- 574
DPI-225	C4 Complement, Chicken anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-032-02
DPI-226	Factor H (Complement), Chicken anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-066-02
DPI-228	Albumin, Human, Chicken anti-	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-026-02
DPI-230	Alpha-1-Acid Glycoprotein, Clone: AGP-47, Mab anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	BYA- 6189-1
DPI-231	0	0	0
DPI-232	Kappa Chain, Mab anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	0
DPI-235	Transthyretin, Prealbuminm, 55kD, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	MED- CLA 193
DPI-237	Transthyretin, Prealbuminm, 55kD, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	MED- CLA 193
DPI-240	Albumin, Human, Chicken anti-	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-026-02
DPI-241	Cystatin C, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	AXL- 574
DPI-244	Apolipoprotein E, LDL, VLDL, Clone: 3D12, Mab anti-Human, frozen/paraffin	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	YM- 5029
DPI-245	Apolipoprotein E, LDL, VLDL, Clone: 3D12, Mab anti-Human, frozen/paraffin	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	YM- 5029
DPI-246	Goat anti-Clusterin (human)	RDI RESEARCH DIAGNOSTICS, INC	RDI-CLUSTRCabG

DPI-247	Transthyretin, Prealbuminm, 55kD, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	MED- CLA 193
DPI-249	C3 Complement, Chicken anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-001-02
DPI-250	Apolipoprotein E, LDL, VLDL, Clone: 3D12, Mab anti-Human, frozen/paraffin	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	YM- 5029
DPI-251	Gelsolin, plasma + cytoplasmic, Sheep anti-	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	YBG- 4628-6210
DPI-252	Apolipoprotein E, LDL, VLDL, Clone: 3D12, Mab anti-Human, frozen/paraffin	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	YM- 5029
DPI-254	C4 Complement, Chicken anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-032-02
DPI-258	C4 Complement, Chicken anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-032-02
DPI-259	Antithrombin III, Clone: BL-ATIII/3, Mab anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	BYA- 9009-1
DPI-261	ANTI-CYTOKERATIN TYPE 10	RDI RESEARCH DIAGNOSTICS, INC	RDI-CBL196
DPI-262	Alpha-1-Acid Glycoprotein, Clone: AGP-47, Mab anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	BYA- 6189-1
DPI-264	Transthyretin, Prealbuminm, 55kD, Rabbit anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	MED- CLA 193
DPI-265	Polylconal Rabbit anti-Human Cytokeratin 1 (Keratin 1)	RDI RESEARCH DIAGNOSTICS, INC	RDI-CYTOK1abr
DPI-267	Monoclonal anti-Prekallikrein Heavy Chain	BIODESIGN INTERNATIONAL	N55199M
DPI-268	C3 Complement, Chicken anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-001-02
DPI-270	Apolipoprotein E, LDL, VLDL, Clone: 3D12, Mab anti-Human, frozen/paraffin	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	YM- 5029
DPI-271	ANTI-CYTOKERATIN TYPE 10	RDI RESEARCH DIAGNOSTICS, INC	RDI-CBL196
DPI-272	RABBIT anti-human INSULIN GROWTH FACTOR BINDING PROTEIN 2	RDI RESEARCH DIAGNOSTICS, INC	RDI-IGFBP2abr
DPI-274	Hemopexin, Beta-1, Rabbit anti-Human, precipitating	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	YN- RHHPX
DPI-279	Monoclonal mouse anti-lactoferrin	RDI RESEARCH DIAGNOSTICS, INC	RDI-TRK4L2-LF2B8
DPI-280	C3 Complement, Chicken anti-Human	ACCURATE CHEMICAL & SCIENTIFIC CORPORATION	IMS- 01-001-02
DPI-281	C4 Complement, Chicken	ACCURATE CHEMICAL &	IMS- 01-032-02

	anti-Human	SCIENTIFIC CORPORATION	

*Further information about these antibodies can be obtained from their commercial sources at: ACCURATE CHEMICAL & SCIENTIFIC CORPORATION http://www.accuratechemical.com/; BIODESIGN INTERNATIONAL - http://www.biodesign.com/; RDI RESEARCH DIAGNOSTICS, INC - http://www.researchd.com/;SANTA CRUZ BIOTECHNOLOGY, INC - http://www.scbt.com/.

In one embodiment, binding of antibody in tissue sections can be used to detect aberrant DPI localization or an aberrant level of one or more DPIs. In a specific embodiment, antibody to a DPI can be used to assay a tissue sample (e.g., a brain biopsy) from a subject for the level of the DPI where an aberrant level of DPI is indicative of BAD. As used herein, an "aberrant level" means a level that is increased or decreased compared with the level in a subject free from BAD or a reference level. If desired, the comparison can be performed with a matched sample from the same subject, taken from a portion of the body not affected by BAD.

Any suitable immunoassay can be used, including, without limitation, competitive and non-competitive assay systems using techniques such as western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoprecipitation assays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, complement-fixation assays, immunoradiometric assays, fluorescent immunoassays and protein A immunoassays.

For example, a DPI can be detected in a fluid sample (e.g., CSF, blood, urine, or tissue homogenate) by means of a two-step sandwich assay. In the first step, a capture reagent (e.g., an anti-DPI antibody) is used to capture the DPI. Examples of such antibodies known in the art are set forth in Table VII. The capture reagent can optionally be immobilized on a solid phase. In the second step, a directly or indirectly labeled detection reagent is used to detect the captured DPI. In one embodiment, the detection reagent is a lectin. Any lectin can be used for this purpose that preferentially binds to the DPI rather than to other isoforms that have the same core protein as the DPI or to other proteins that share the antigenic determinant recognized by the antibody. In a preferred embodiment, the chosen lectin binds to the DPI with at least 2-fold greater affinity, more preferably at least 5-fold greater affinity, still more preferably at least 10- fold greater affinity, than to said other isoforms that have the same core protein as the DPI or to said other proteins that share the antigenic determinant recognized by the antibody. Based on the present description, a lectin

that is suitable for detecting a given DPI can readily be identified by methods well known in the art, for instance upon testing one or more lectins enumerated in Table I on pages 158-159 of Sumar et al., Lectins as Indicators of Disease-Associated Glycoforms, In: Gabius H-J & Gabius S (eds.), 1993, Lectins and Glycobiology, at pp. 158-174 (which is incorporated herein by reference in its entirety). Lectins with the desired oligosaccharide specificity can be identified, for example, by their ability to detect the DPI in a 2D gel, in a replica of a 2D gel following transfer to a suitable solid substrate such as a nitrocellulose membrane, or in a two-step assay following capture by an antibody. In an alternative embodiment, the detection reagent is an antibody, e.g., an antibody that immunospecifically detects other post- translational modifications, such as an antibody that immunospecifically binds to phosphorylated amino acids. Examples of such antibodies include those that bind to phosphotyrosine (BD Transduction Laboratories, catalog nos.: P11230-050/P11230- 150; P11120; P38820; P39020), those that bind to phosphoserine (Zymed Laboratories Inc., South San Francisco, CA, catalog no. 61-8100) and those that bind to phosphothreonine (Zymed Laboratories Inc., South San Francisco, CA, catalog nos. 71- 8200, 13-9200).

If desired, a gene encoding a DPI, a related gene, or related nucleic acid sequences or subsequences, including complementary sequences, can also be used in hybridization assays. A nucleotide encoding a DPI, or subsequences thereof comprising at least 8 nucleotides, preferably at least 12 nucleotides, and most preferably at least 15 nucleotides can be used as a hybridization probe. Hybridization assays can be used for detection, prognosis, diagnosis, or monitoring of conditions, disorders, or disease states, associated with aberrant expression of genes encoding DPIs, or for differential diagnosis of subjects with signs or symptoms suggestive of BAD. In particular, such a hybridization assay can be carried out by a method comprising contacting a subject's sample containing nucleic acid with a nucleic acid probe capable of hybridizing to a DNA or RNA that encodes a DPI, under conditions such that hybridization can occur, and detecting or measuring any resulting hybridization. Nucleotides can be used for therapy of subjects having BAD, as described below.

The methods and compositions for clinical screening, diagnosis and prognosis of BAD in a mammalian subject may be diagnostic of BAD or indicative of BAD.

Diagnostic methods and compositions are based on Depression-Associated Features (DFs) and Depression-Associated Protein Isoforms (DPIs) which are

specifically and particularly associated with BAD and are generally not associated with other diseases or conditions. Such diagnostic DFs or DPIs, which are specifically associated with BAD, are useful in screening, diagnosis and prognosis as indicators of BAD. The administration of therapeutic compositions which are directed against or lead to modulation of diagnostic markers may have therapeutic value particularly in BAD.

Indicative methods and compositions are based on Depression-Associated Features (DFs) and Depression-Associated Protein Isoforms (DPIs) which are associated with BAD but may not be specific only for BAD, and may be associated with one or more other diseases or conditions. Such indicative DFs or DPIs, which are associated with BAD, but not only with BAD, are useful in screening, diagnosis and prognosis as indicators of BAD. Indicative methods and compositions are particularly useful in the initial or general screening, diagnosis and prognosis of an individual subject, whereby a first indication of a subset of conditions or diseases, including BAD, is thereby provided. Additional assessment utilizing diagnostic or particular BAD DFs or DPIs may then be undertaken to provide specific, diagnostic screening, diagnosis and prognosis of the individual subject. The administration of therapeutic compositions which are directed against or lead to modulation of indicative markers may have therapeutic value in BAD and other disorders as well, or may be useful therapeutically in more than one disease or condition.

Thus, a diagnostic marker changes (increases, decreases or otherwise alters form or character) significantly in only a single disease or condition or in only a small number of conditions, particularly in related conditions. One such diagnostic marker, DF-60, is provided below in Table VIII.

Table VIII: Example of a diagnostic marker for BAD:

Feature #	Isoform #	Fold Change	pI	MW (Da)
DF-60	DPI-38	-2.33	6.05	47450

An indicative marker changes (increases, decreases or otherwise alters form or character) significantly in more than one condition, particularly in BAD and one or more other distinct diseases or conditions. One such indicative marker, DF-155, is found to increase in BAD and is provided in Table IX. This same marker, identified or characterised by the same pI and MW, is noted as SF-255 as similarly found to be

increased in Schizophrenia. The DF-155/SF-255 marker is therefore indicative of Depression and/or Schizophrenia.

Table IX: Example of an indicative marker for BAD:

Feature #	Isoform #	Disease	Fold Change	pI	MW (Da)
DF-155	DPI-93	Depression	1.92	7.03	155828
SF-255	SPI-138	Schizophrenia	2.25	7.03	155828

The invention also provides diagnostic kits, comprising an anti-DPI antibody. In addition, such a kit may optionally comprise one or more of the following: (1) instructions for using the anti-DPI antibody for diagnosis, prognosis, therapeutic monitoring or any combination of these applications; (2) a labeled binding partner to the antibody; (3) a solid phase (such as a reagent strip) upon which the anti-DPI antibody is immobilized; and (4) a label or insert indicating regulatory approval for diagnostic, prognostic or therapeutic use or any combination thereof. If no labeled binding partner to the antibody is provided, the anti-DPI antibody itself can be labeled with a detectable marker, e.g., a chemiluminescent, enzymatic, fluorescent, or radioactive moiety.

The invention also provides a kit comprising a nucleic acid probe capable of hybridizing to RNA encoding a DPI. In a specific embodiment, a kit comprises in one or more containers a pair of primers (e.g., each in the size range of 6-30 nucleotides, more preferably 10-30 nucleotides and still more preferably 10-20 nucleotides) that under appropriate reaction conditions can prime amplification of at least a portion of a nucleic acid encoding a DPI, such as by polymerase chain reaction (see, e.g., Innis et al., 1990, PCR Protocols, Academic Press, Inc., San Diego, CA), ligase chain reaction (see EP 320,308) use of Qβ replicase, cyclic probe reaction, or other methods known in the art.

Kits are also provided which allow for the detection of a plurality of DPIs or a plurality of nucleic acids each encoding a DPI. A kit can optionally further comprise a predetermined amount of an isolated DPI protein or a nucleic acid encoding a DPI, e.g., for use as a standard or control.

5.3 Statistical Techniques for Identifying DPIs and DPI Clusters

The uni-variate differential analysis tools, such as fold changes, wilcoxon rank sum test and t-test, are useful in identifying individual DFs or DPIs that are diagnostically associated with BAD or in identifying individual DPIs that regulate the disease process. In most cases, however, those skilled in the art appreciate that the disease process is associated with a combination of DFs or DPIs (and to be regulated by a combination of DPIs), rather than individual DFs and DPIs in isolation. The strategies for discovering such combinations of DFs and DPIs differ from those for discovering individual DFs and DPIs. In such cases, each individual DF and DPI can be regarded as one variable and the disease can be regarded as a joint, multi-variate effect caused by interaction of these variables.

The following steps can be used to identify markers from data produced by the Preferred Technology.

The first step is to identify a collection of DFs or DPIs that individually show significant association with BAD. The association between the identified DFs or DPIs and BAD need not be as highly significant as is desirable when an individual DF or DPI is used as a diagnostic. Any of the tests discussed above (fold changes, wilcoxon rank sum test, etc.) can be used at this stage. Once a suitable collection of DFs or DPIs has been identified, a sophisticated multi-variate analysis capable of identifying clusters can then be used to estimate the significant multivariate associations with BAD.

Linear Discriminant Analysis (LDA) is one such procedure, which can be used to detect significant association between a cluster of variables (i.e., DFs or DPIs) and BAD. In performing LDA, a set of weights is associated with each variable (i.e., DF or DPI) so that the linear combination of weights and the measured values of the variables can identify the disease state by discriminating between subjects having BAD and subjects free from BAD. Enhancements to the LDA allow stepwise inclusion (or removal) of variables to optimize the discriminant power of the model. The result of the LDA is therefore a cluster of DFs or DPIs which can be used for diagnosis, prognosis, therapy or drug development. Other enhanced variations of LDA, such as Flexible Discriminant Analysis permit the use of non-linear combinations of variables to discriminate a disease state from a normal state. The results of the discriminant analysis can be verified by post-hoc tests and also by repeating the analysis using alternative techniques such as classification trees.

A further category of DFs or DPIs can be identified by qualitative measures by comparing the percentage feature presence of an DF or DPI of one group of samples (e.g., samples from diseased subjects) with the percentage feature presence of an DF or DPI in another group of samples (e.g., samples from control subjects). The "percentage feature presence" of an DF or DPI is the percentage of samples in a group of samples in which the DF or DPI is detectable by the detection method of choice. For example, if an DF is detectable in 95 percent of samples from diseased subjects, the percentage feature presence of that DF in that sample group is 95 percent. If only 5 percent of samples from non-diseased subjects have detectable levels of the same DF, detection of that DF in the sample of a subject would suggest that it is likely that the subject suffers from BAD.

5.4 Use in Clinical Studies

The diagnostic methods and compositions of the present invention can assist in monitoring a clinical study, e.g. to evaluate drugs for therapy of BAD. In one embodiment, candidate molecules are tested for their ability to restore DF or DPI levels in a subject having BAD to levels found in subjects free from BAD or, in a treated subject (e.g. after treatment with mood stabilizers: lithium, divalproex, carbamazepine, lamotrigine; antidepressants: tricyclic antidepressants (e.g. Desipramine, chlorimipramine, nortriptyline), selective serotonin reuptake inhibitors (SSRIs including fluoxetine (Prozac), sertraltrine (Zoloft), paroxitene (Paxil), fluvoxamine (Luvox), and citalopram (Celexa)), MAOIs, bupropion (Wellbutrin), venlafaxine (Effexor), and mirtazapine (Remeron); and atypical antipsychotic agents: Clozapine, Olanzapine, Risperidone), to preserve DF or DPI levels at or near non-BAD values. The levels of one or more DFs or DPIs can be assayed.

In another embodiment, the methods and compositions of the present invention are used to screen candidates for a clinical study to identify individuals having BAD; such individuals can then be excluded from the study or can be placed in a separate cohort for treatment or analysis. If desired, the candidates can concurrently be screened to identify individuals with attention deficit disorder, a schizoaffective disorder or a unipolar affective disorder.

5.5 Purification of DPIs

In particular aspects, the invention provides isolated mammalian DPIs, preferably human DPIs, and fragments thereof which comprise an antigenic determinant (i.e., can be recognized by an antibody) or which are otherwise functionally active, as well as nucleic acid sequences encoding the foregoing. "Functionally active" as used herein refers to material displaying one or more functional activities associated with a full-length (wild- type) DPI, e.g., binding to a DPI substrate or DPI binding partner, antigenicity (binding to an anti-DPI antibody), immunogenicity, enzymatic activity and the like.

In specific embodiments, the invention provides fragments of a DPI comprising at least 5 amino acids, at least 10 amino acids, at least 50 amino acids, or at least 75 amino acids. Fragments lacking some or all of the regions of a DPI are also provided, as are proteins (e.g., fusion proteins) comprising such fragments. Nucleic acids encoding the foregoing are provided.

Once a recombinant nucleic acid which encodes the DPI, a portion of the DPI, or a precursor of the DPI is identified, the gene product can be analyzed. This is achieved by assays based on the physical or functional properties of the product, including radioactive labeling of the product followed by analysis by gel electrophoresis, immunoassay, etc.

The DPIs identified herein can be isolated and purified by standard methods including chromatography (e.g., ion exchange, affinity, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins.

Alternatively, once a recombinant nucleic acid that encodes the DPI is identified, the entire amino acid sequence of the DPI can be deduced from the nucleotide sequence of the gene coding region contained in the recombinant nucleic acid. As a result, the protein can be synthesized by standard chemical methods known in the art (e.g., see Hunkapiller et al., 1984, Nature 310:105-111).

In another alternative embodiment, native DPIs can be purified from natural sources, by standard methods such as those described above (e.g., immunoaffinity purification).

In a preferred embodiment, DPIs are isolated by the Preferred Technology described supra. For preparative-scale runs, a narrow-range "zoom gel" having a pH range of 2 pH units or less is preferred for the isoelectric step, according to the method described in Westermeier, 1993, Electrophoresis in Practice (VCH,

Weinheim, Germany), pp. 197-209 (which is incorporated herein by reference in its entirety); this modification permits a larger quantity of a target protein to be loaded onto the gel, and thereby increases the quantity of isolated DPI that can be recovered from the gel. When used in this way for preparative- scale runs, the Preferred Technology typically provides up to 100 ng, and can provide up to 1000 ng, of an isolated DPI in a single run. Those of skill in the art will appreciate that a zoom gel can be used in any separation strategy which employs gel isoelectric focusing.

The invention thus provides an isolated DPI, an isolated DPI-related polypeptide, and an isolated derivative or fragment of a DPI or a DPI-related polypeptide; any of the foregoing can be produced by recombinant DNA techniques or by chemical synthetic methods.

5.6 Isolation of DNA Encoding a DPI

Specific embodiments for the cloning of a gene encoding a DPI, are presented below by way of example and not of limitation.

The nucleotide sequences of the present invention, including DNA and RNA, and comprising a sequence encoding a DPI or a fragment thereof, or a DPI-related polypeptide, may be synthesized using methods known in the art, such as using conventional chemical approaches or polymerase chain reaction (PCR) amplification. The nucleotide sequences of the present invention also permit the identification and cloning of the gene encoding a DPI homolog or DPI ortholog including, for example, by screening cDNA libraries, genomic libraries or expression libraries.

For example, to clone a gene encoding a DPI by PCR techniques, anchored degenerate oligonucleotides (or a set of most likely oligonucleotides) can be designed for all DPI peptide fragments identified as part of the same protein. PCR reactions under a variety of conditions can be performed with relevant cDNA and genomic DNAs (e.g., from brain tissue or from cells of the immune system) from one or more species. Also vectorette reactions can be performed on any available cDNA and genomic DNA using the oligonucleotides (which preferably are nested) as above. Vectorette PCR is a method that enables the amplification of specific DNA fragments in situations where the sequence of only one primer is known. Thus, it extends the application of PCR to stretches of DNA where the sequence information is only available at one end. (Arnold C, 1991, PCR Methods Appl. 1(1):39-42; Dyer KD, Biotechniques, 1995, 19(4):550-2). Vectorette PCR may pe performed with probes

that are, for example, anchored degenerate oligonucleotides (or most likely oligonucleotides) coding for DPI peptide fragments, using as a template a genomic library or cDNA library pools.

Anchored degenerate oligonucleotides (and most likely oligonucleotides) can be designed for all DPI peptide fragments. These oligonucleotides may be labelled and hybridized to filters containing cDNA and genomic DNA libraries. Oligonucleotides to different peptides from the same protein will often identify the same members of the library. The cDNA and genomic DNA libraries may be obtained from any suitable or desired mammalian species, for example from humans.

Nucleotide sequences comprising a nucleotide sequence encoding a DPI or DPI fragment of the present invention are useful for their ability to hybridize selectively with complementary stretches of genes encoding other proteins. Depending on the application, a variety of hybridization conditions may be employed to obtain nucleotide sequences at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or 99% identical, or 100% identical, to the sequence of a nucleotide encoding a DPI.

For a high degree of selectivity, relatively stringent conditions are used to form the duplexes, such as low salt or high temperature conditions. As used herein, "highly stringent conditions" means hybridization to filter-bound DNA in 0.5 M NaHPO4, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65 °C, and washing in 0.1xSSC/0.1% SDS at 68 °C (Ausubel F.M. et al., eds., 1989, Current Protocols in Molecular Biology, Vol. I, Green Publishing Associates, Inc., and John Wiley & Sons, Inc., New York, at p. 2.10.3; incorporated herein by reference in its entirety.) For some applications, less stringent conditions for duplex formation are required. As used herein "moderately stringent conditions" means washing in 0.2xSSC/0.1% SDS at 42 °C (Ausubel et al., 1989, supra). Hybridization conditions can also be rendered more stringent by the addition of increasing amounts of formamide, to destabilize the hybrid duplex. Thus, particular hybridization conditions can be readily manipulated, and will generally be chosen depending on the desired results. In general, convenient hybridization temperatures in the presence of 50% formamide are: 42 °C for a probe which is 95 to 100% identical to the fragment of a gene encoding a DPI, 37 °C for 90 to 95% identity and 32 °C for 70 to 90% identity.

In the preparation of genomic libraries, DNA fragments are generated, some of which will encode parts or the whole of a DPI. Any suitable method for preparing DNA fragments may be used in the present invention. For example, the DNA may be cleaved at specific sites using various restriction enzymes. Alternatively, one may use DNAse in the presence of manganese to fragment the DNA, or the DNA can be physically sheared, as for example, by sonication. The DNA fragments can then be separated according to size by standard techniques, including but not limited to agarose and polyacrylamide gel electrophoresis, column chromatography and sucrose gradient centrifugation. The DNA fragments can then be inserted into suitable vectors, including but not limited to plasmids, cosmids, bacteriophages lambda or T4, and yeast artificial chromosome (YAC). (See, e.g., Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York; Glover, D.M. (ed.), 1985, DNA Cloning: A Practical Approach, MRL Press, Ltd., Oxford, U.K. Vol. I, II; Ausubel F.M. et al., eds., 1989, Current Protocols in Molecular Biology, Vol. I, Green Publishing Associates, Inc., and John Wiley & sons, Inc., New York). The genomic library may be screened by nucleic acid hybridization to labeled probe (Benton and Davis, 1977, Science 196:180; Grunstein and Hogness, 1975, Proc. Natl. Acad. Sci. U.S.A. 72:3961).

Based on the present description, the genomic libraries may be screened with labeled degenerate oligonucleotide probes corresponding to the amino acid sequence of any peptide of the DPI using optimal approaches well known in the art. Any probe used is at least 10 nucleotides, at least 15 nucleotides, at least 20 nucleotides, at least 25 nucleotides, at least 30 nucleotides, at least 40 nucleotides, at least 50 nucleotides, at least 60 nucleotides, at least 70 nucleotides, at least 80 nucleotides, or at least 100 nucleotides. Preferably a probe is 10 nucleotides or longer, and more preferably 15 nucleotides or longer.

In Tables IV and V above, some DPIs disclosed herein correspond to isoforms of previously identified proteins encoded by genes whose sequences are publicly known. To screen such a gene, any probe may be used that is complementary to the gene or its complement; preferably the probe is 10 nucleotides or longer, more preferably 15 nucleotides or longer. The SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at http://www.expasy.ch/) and the GenBank database (held by the National Institute of Health (NIH) which is available at

http://www.ncbi.nlm.nih.gov/) provide protein sequences for the DPIs listed in Tables IV and V under the following accession numbers and each sequence is incorporated herein by reference:

Table X. Nucleotide sequences encoding DPIs, DPI Related Proteins or ERPIs

DF#	DPI#	Accession Numbers of Identified Sequences
DF-3	DPI-139	P02790
DF-3	DPI-140	P02768
DF-4	DPI-2	7662374
DF-6	DPI-141	P41222
DF-7	DPI-3	P01034
DF-8	DPI-4	P41222
DF-9	DPI-103	5729767
DF-10	DPI-5	P01028
DF-11	DPI-142	Q99963
DF-14	DPI-104	P41222
DF-17	DPI-105	P01023
DF-18	DPI-6	7019363, 6469030
DF-19	DPI-106	P01023
DF-22	DPI-7	P02765
DF-23	DPI-143	P01876
DF-24	DPI-107	P54289
DF-25	DPI-8	P02649
DF-25	DPI-108	P02766
DF-26	DPI-144	P02763
DF-28	DPI-9	P01028
DF-29	DPI-10	P01034
DF-30	DPI-11	P04217
DF-31	DPI-12	P00734
DF-33	DPI-13	P10909
DF-34	DPI-109	P01034
DF-35	DPI-145	P13645
DF-36	DPI-14	P01034
DF-37	DPI-15	P01008
DF-37	DPI-110	P02766
DF-39	DPI-17	P05067
DF-39	DPI-18	P05155

DF-40	DPI-19	P02649
DF-40	DPI-20	P10909
DF-41	DPI-21	7662374
DF-41	DPI-111	P13591
DF-42	DPI-22	P02765
DF-43	DPI-23	P01024
DF-43	DPI-24	P05546
DF-44	DPI-25	P05067
DF-51	DPI-29	P06396
DF-52	DPI-30	P00751
DF-55	DPI-34	P36955
DF-55	DPI-113	P02768
DF-56	DPI-35	P06396
DF-58	DPI-37	P09871
DF-60	DPI-38	P36955
DF-61	DPI-39	Q92876
DF-64	DPI-44	P01011
DF-65	DPI-45	NOVEL (cloned)
DF-65	DPI-146	P01019
DF-66	DPI-47	P41222
DF-67	DPI-115	P02768
DF-68	DPI-49	P36222
DF-69	DPI-50	P41222
DF-70	DPI-51	P01024
DF-70	DPI-116	P10909
DF-71	DPI-52	P41222
DF-76	DPI-57	P02023
DF-77	DPI-58	P00915
DF-78	DPI-147	P06733
DF-82	DPI-151	P02024
DF-82	DPI-152	1095700.4; AK021499.1
DF-84	DPI-154	P01922
DF-84	DPI-155	P01034
DF-86	DPI-59	P05090
DF-87	DPI-60	P50446
DF-94	DPI-65	P01034
DF-94	DPI-119	P02023
DF-95	DPI-159	P02023; P02024

DF-96	DPI-66	P01034
DF-97	DPI-160	P02023
DF-97	DPI-161	P01034
DF-100	DPI-162	P04040
DF-101	DPI-67	P01028
DF-102	DPI-163	P02023, P02024
DF-102	DPI-164	475127.2
DF-102	DPI-165	19063.1
DF-102	DPI-166	P18519
DF-103	DPI-69	P32119
DF-104	DPI-167	Q92740
DF-104	DPI-168	P04004
DF-104	DPI-169	P41222
DF-105	DPI-170	Q09054
DF-106	DPI-120	P05090
DF-106	DPI-121	P09486
DF-107	DPI-171	P02023, P02024
DF-108	DPI-172	P02023, P02024
DF-110	DPI-173	P02023, P02024
DF-112	DPI-174	P06732
DF-115	DPI-71	P02675
DF-118	DPI-175	P06396
DF-120	DPI-123	P35908
DF-123	DPI-72	P02766
DF-124	DPI-176	P09211
DF-125	DPI-73	P02768
DF-127	DPI-177	P06396
DF-130	DPI-178	P06733
DF-131	DPI-76	P02675
DF-134	DPI-78	P15169
DF-134	DPI-124	4557617
DF-135	DPI-79	P02570
DF-137	DPI-179	P13645
DF-138	DPI-87	P06727
DF-142	DPI-181	P02790
DF-144	DPI-127	P10909
DF-144	DPI-128	P05090
DF-144	DPI-129	P02790

DF-145	DPI-88	P01344
DF-146	DPI-89	P01028
DF-148	DPI-90	P01871
DF-153	DPI-92	P06727
DF-155	DPI-93	Q02246
DF-158	DPI-184	P36222
DF-161	DPI-96	P17174
DF-164	DPI-135	P04217
DF-170	DPI-185	P41222
DF-172	DPI-186	8918224
DF-174	DPI-187	P01019
DF-176	DPI-188	P05067
DF-178	DPI-189	P01034
DF-179	DPI-190	P10909
DF-180	DPI-191	2745741
DF-188	DPI-192	8918224
DF-189	DPI-193	P41222
DF-190	DPI-194	P05067
DF-194	DPI-195	P05090
DF-197	DPI-196	P05090
DF-198	DPI-197	2117873
DF-200	DPI-198	P16035
DF-201	DPI-199	P01028
DF-202	DPI-200	P02768
DF-203	DPI-201	P10909
DF-204	DPI-202	P05090
DF-207	DPI-203	P00441
DF-208	DPI-204	P41222
DF-210	DPI-205	Q99435
DF-211	DPI-206	P05067
DF-213	DPI-207	P07339
DF-213	DPI-208	P02774
DF-213	DPI-209	P02768
DF-213	DPI-210	2745741
DF-214	DPI-211	P05067
DF-215	DPI-212	P01008
DF-215	DPI-213	NOVEL
DF-216	DPI-214	P10909

DF-217	DPI-215	P10909
DF-218	DPI-216	P05090
DF-220	DPI-217	M16961.1
DF-222	DPI-218	6651381
DF-224	DPI-219	P01023
DF-225	DPI-220	D16469.1
DF-226	DPI-221	P41222
DF-227	DPI-222	P01023
DF-231	DPI-223	P01028
DF-235	DPI-224	P01034
DF-236	DPI-225	P01028
DF-237	DPI-226	Q03591
DF-239	DPI-227	P41222
DF-239	DPI-228	P02768
DF-240	DPI-229	7662374
DF-261	DPI-230	P02763
DF-262	DPI-231	229528
DF-262	DPI-232	P00918
DF-265	DPI-233	P41222
DF-266	DPI-234	P36222
DF-269	DPI-235	P02766
DF-271	DPI-236	P41222
DF-273	DPI-237	P02766
DF-275	DPI-238	Q01469
DF-281	DPI-239	P02748
DF-282	DPI-240	P02768
DF-283	DPI-241	P01034
DF-286	DPI-242	P05413
DF-287	DPI-243	P41222
DF-288	DPI-244	P02649
DF-289	DPI-245	P02649
DF-289	DPI-246	P10909
DF-289	DPI-247	P02766
DF-291	DPI-248	P41222
DF-295	DPI-249	P01024
DF-297	DPI-250	P02649
DF-299	DPI-251	P06396
DF-300	DPI-252	P02649

DF-302	DPI-253	1096891
DF-303	DPI-254	P01028
DF-306	DPI-255	P30041
DF-310	DPI-256	P01023
DF-311	DPI-257	P41222
DF-313	DPI-258	P01028
DF-316	DPI-259	P01008
DF-322	DPI-260	P41222
DF-323	DPI-261	P13645
DF-326	DPI-262	P02763
DF-326	DPI-263	O14791
DF-327	DPI-264	P02766
DF-329	DPI-265	P04264
DF-330	DPI-266	P25311
DF-332	DPI-267	P29622
DF-334	DPI-268	P01024
DF-335	DPI-269	Q12805
DF-342	DPI-270	P02649
DF-343	DPI-271	P13645
DF-343	DPI-272	P18065
DF-347	DPI-273	P41222
DF-349	DPI-274	P02790
DF-351	DPI-275	P41222
DF-353	DPI-276	AF192968.1
DF-355	DPI-277	P01023
DF-356	DPI-278	P23142
DF-357	DPI-279	P09571
DF-357	DPI-280	P01024
DF-358	DPI-281	P01028
ERF-1	ERPI-1	P01028
ERF-2	ERPI-2	P04217

For DPI-45 and DPI-213, the partial sequence information derived from tandem mass spectrometry was not found to be described as a transcribed protein in any known public database. DPI-45 and DPI-213 are therefore listed as 'NOVEL' in Table X. DPI-45 and DPI-213 have been cloned, and is further described below. For any DPI, degenerate probes, or probes taken from the sequences described above by

accession number may be used for screening. In the case of degenerate probes, they can be constructed from the partial amino sequence information obtained from tandem mass spectra of tryptic digest peptides of the DPI. To screen such a gene, any probe may be used that is complementary to the gene or its complement; preferably the probe is 10 nucleotides or longer, more preferably 15 nucleotides or longer.

When a library is screened, clones with insert DNA encoding the DPI or a fragment thereof will hybridize to one or more members of the corresponding set of degenerate oligonucleotide probes (or their complement). Hybridization of such oligonucleotide probes to genomic libraries is carried out using methods known in the art. For example, hybridization with one of the above-mentioned degenerate sets of oligonucleotide probes, or their complement (or with any member of such a set, or its complement) can be performed under highly stringent or moderately stringent conditions as defined above, or can be carried out in 2X SSC, 1.0% SDS at 50 °C and washed using the washing conditions described supra for highly stringent or moderately stringent hybridization.

In yet another aspect of the invention, clones containing nucleotide sequences encoding the entire DPI, a fragment of a DPI, a DPI-related polypeptide, or a fragment of a DPI-related polypeptide or any of the foregoing may also be obtained by screening expression libraries. For example, DNA from the relevant source is isolated and random fragments are prepared and ligated into an expression vector (e.g., a bacteriophage, plasmid, phagemid or cosmid) such that the inserted sequence in the vector is capable of being expressed by the host cell into which the vector is then introduced. Various screening assays can then be used to select for the expressed DPI or DPI-related polypeptides. In one embodiment, the various anti-DPI antibodies of the invention can be used to identify the desired clones using methods known in the art. See, for example, Harlow and Lane, 1988, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, Appendix IV. Colonies or plaques from the library are brought into contact with the antibodies to identify those clones that bind antibody.

In an embodiment, colonies or plaques containing DNA that encodes a DPI, a fragment of a DPI, a DPI-related polypeptide, or a fragment of a DPI-related polypeptide can be detected using DYNA Beads according to Olsvick et al., 29th ICAAC, Houston, Tex. 1989, incorporated herein by reference. Anti-DPI antibodies

are crosslinked to tosylated DYNA Beads M280, and these antibody-containing beads are then contacted with colonies or plaques expressing recombinant polypeptides. Colonies or plaques expressing a DPI or DPI-related polypeptide are identified as any of those that bind the beads.

Alternatively, the anti-DPI antibodies can be nonspecifically immobilized to a suitable support, such as silica or Celite® resin. This material is then used to adsorb to bacterial colonies expressing the DPI protein or DPI-related polypeptide as described herein.

In another aspect, PCR amplification may be used to isolate from genomic DNA a substantially pure DNA (i.e., a DNA substantially free of contaminating nucleic acids) encoding the entire DPI or a part thereof. Preferably such a DNA is at least 95% pure, more preferably at least 99% pure. Oligonucleotide sequences, degenerate or otherwise, that correspond to peptide sequences of DPIs disclosed herein can be used as primers.

PCR can be carried out, e.g., by use of a Perkin-Elmer Cetus thermal cycler and Taq polymerase (Gene Amp® or AmpliTaq DNA polymerase). One can choose to synthesize several different degenerate primers, for use in the PCR reactions. It is also possible to vary the stringency of hybridization conditions used in priming the PCR reactions, to allow for greater or lesser degrees of nucleotide sequence similarity between the degenerate primers and the corresponding sequences in the DNA. After successful amplification of a segment of the sequence encoding a DPI, that segment may be molecularly cloned and sequenced, and utilized as a probe to isolate a complete genomic clone. This, in turn, will permit the determination of the gene's complete nucleotide sequence, the analysis of its expression, and the production of its protein product for functional analysis, as described infra.

The gene encoding a DPI can also be identified by mRNA selection by nucleic acid hybridization followed by *in vitro* translation. In this procedure, fragments are used to isolate complementary mRNAs by hybridization. Such DNA fragments may represent available, purified DNA encoding a DPI of another species (e.g., mouse, human). Immunoprecipitation analysis or functional assays (e.g., aggregation ability *in vitro*; binding to receptor) of the *in vitro* translation products of the isolated products of the isolated mRNAs identifies the mRNA and, therefore, the complementary DNA fragments that contain the desired sequences. In addition, specific mRNAs may be selected by adsorption of polysomes isolated from cells to

immobilized antibodies that specifically recognize a DPI. A radiolabelled cDNA encoding a DPI can be synthesized using the selected mRNA (from the adsorbed polysomes) as a template. The radiolabelled mRNA or cDNA may then be used as a probe to identify the DNA fragments encoding a DPI from among other genomic DNA fragments.

Alternatives to isolating genomic DNA encoding a DPI include, but are not limited to, chemically synthesizing the gene sequence itself from a known sequence or making cDNA to the mRNA which encodes the DPI. For example, RNA for cDNA cloning of the gene encoding a DPI can be isolated from cells which express the DPI. Those skilled in the art will understand from the present description that other methods may be used and are within the scope of the invention.

Any suitable eukaryotic cell can serve as the nucleic acid source for the molecular cloning of the gene encoding a DPI. The nucleic acid sequences encoding the DPI can be isolated from vertebrate, mammalian, primate, human, porcine, bovine, feline, avian, equine, canine or murine sources. The DNA may be obtained by standard procedures known in the art from cloned DNA (e.g., a DNA "library"), by chemical synthesis, by cDNA cloning, or by the cloning of genomic DNA, or fragments thereof, purified from the desired cell. (See, e.g., Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York; Glover, D.M. (ed.), 1985; DNA Cloning: A Practical Approach, MRL Press, Ltd., Oxford, U.K. Vol. I, II.) Clones derived from genomic DNA may contain regulatory and intron DNA regions in addition to coding regions; clones derived from cDNA will contain only exon sequences.

The identified and isolated gene or cDNA can then be inserted into any suitable cloning vector. A large number of vector-host systems known in the art may be used. As those skilled in the art will appreciate, the only limitation is that the vector system chosen be compatible with the host cell used. Such vectors include, but are not limited to, bacteriophages such as lambda derivatives, plasmids such as PBR322 or pUC plasmid derivatives or the Bluescript vector (Stratagene) or modified viruses such as adenoviruses, adeno-associated viruses or retroviruses. The insertion into a cloning vector can be accomplished, for example, by ligating the DNA fragment into a cloning vector which has complementary cohesive termini. However, if the complementary restriction sites used to fragment the DNA are not present in the cloning vector, the ends of the DNA molecules may be enzymatically modified.

Alternatively, any site desired may be produced by ligating nucleotide sequences (linkers) onto the DNA termini; these ligated linkers may comprise specific chemically synthesized oligonucleotides encoding restriction endonuclease recognition sequences. In an alternative method, the cleaved vector and the gene encoding a DPI may be modified by homopolymeric tailing. Recombinant molecules can be introduced into host cells via transformation, transfection, infection, electroporation, etc., so that many copies of the gene sequence are generated.

In specific embodiments, transformation of host cells with recombinant DNA molecules that incorporate the isolated gene encoding the DPI, cDNA, or synthesized DNA sequence enables generation of multiple copies of the gene. Thus, the gene may be obtained in large quantities by growing transformants, isolating the recombinant DNA molecules from the transformants and, when necessary, retrieving the inserted gene from the isolated recombinant DNA.

The nucleotide sequences of the present invention include nucleotide sequences encoding amino acid sequences with substantially the same amino acid sequences as native DPIs, nucleotide sequences encoding amino acid sequences with functionally equivalent amino acids, nucleotide sequences encoding DPIs, a fragments of DPIs, DPI-related polypeptides, or fragments of DPI-related polypeptides.

In a specific embodiment, an isolated nucleic acid molecule encoding a DPI-related polypeptide can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of a DPI such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Standard techniques known to those of skill in the art can be used to introduce mutations, including, for example, site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a side chain with a similar charge. Families of amino acid residues having side chains with similar charges have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine,

tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Alternatively, mutations can be introduced randomly along all or part of the coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for biological activity to identify mutants that retain activity. Following mutagenesis, the encoded protein can be expressed and the activity of the protein can be determined.

5.6.1 Cloning and Characterization of DPI-45 and DPI-213

DPI-45 and DPI-213 were isolated, subjected to proteolysis, and analyzed by mass spectrometry using the methods and apparatus of the Preferred Technology. Using the SEQUEST search program as described in the Examples, infra, uninterpreted tandem mass spectra of tryptic digest peptides were searched against a database of public domain proteins constructed of protein entries in the non-redundant database held by the National Centre for Biotechnology Information (NCBI) which is accessible at http://www.ncbi.nlm.nih.gov/ and also constructed of Expressed Sequence Tags entries (http://www.ncbi.nlm.nih.gov/dbEST/index.html). As a result of database searching, the following amino acid sequence of a tryptic digest peptide of both DPI-45 and DPI-213 was determined from a match to a tryptic digest peptide in a conceptual translation of EST AA326679: EWVAIESDSVQPVPR (shown in Figure 2B).

In cases where no amino acid sequences could be determined through searching using the SEQUEST program, tandem mass spectra of the peptides were interpreted manually, using methods known in the art as described in the Examples, infra. In the method of tandem mass spectrometry used for sequencing peptides in the present invention, the following pairs of amino acids could not be distinguished from each other: leucine and isoleucine; and, under certain circumstances, glutamine and lysine, and phenylalanine and oxidized methionine. As used herein, an amino acid sequence "as determined by mass spectrometry" refers to the set of amino acid sequences containing at the indicated positions, one or other member of the designated pairs of amino acids. For example, the amino acid sequence P[L/I]A indicates the amino acid sequences PLA and PIA. As will be obvious to one of skill in the art, a sequence containing n designated pairs indicates 2^n amino acid sequences. In

Table XI, each possible amino acid sequence is listed for each sequence determined by mass spectrometry.

Table XI. Partial Amino Acid Sequences of DPI-45 and DPI-213 as Determined by Mass Spectrometry

DF#	DPI#	Mass of peptide analyzed by mass spectrometry*	Partial amino acid sequences	Mass to N-terminus	Mass to C-terminus	pI	MW
DF-65	DPI-45	1258.65	H[L/I]D[L/I]EEYR	184.07	0.00	4.86	60009
DF-215	DPI-213	1258.65	H[L/I]D[L/I]EEYR	184.07	0.00	5.04	57690

*The masses determined by mass spectrometry have an error of mass measurement of 100 parts-per-million (ppm) or less. For a given measured mass, *M*, having an error of mass measurement of *z* ppm, the error of mass measurement can be calculated as (*M* x z ÷1000000).

As used herein, the "mass of the peptide analyzed by mass spectrometry" is the mass of the singly protonated peptide measured by mass spectrometry, and corresponds to the total mass of the constituent amino acid residues of the peptide with the addition of a water molecule (H2O) and a single proton (H+). As used herein, the "mass to N- terminus" corresponds to the total mass of the constituent amino acid residues extending from the start of the partial sequence to the N-terminus of the peptide. As used herein, the "mass to C-terminus" corresponds to the total mass of the constituent amino acid residues extending from the end of the partial sequence to the C-terminus of the peptide with the addition of a water molecular (H2O), and a single proton (H+).

The partial amino acid sequence and masses listed in Table XI were not found to match to any sequences in the database used.

EST AA326679 shows 44% amino acid identity with a putative human protein derived from a conceptual translation of the cDNA CAB07646.1 (available at http://www.ncbi.nlm.nih.gov/entrez/). The C terminus of this protein sequence (CAB07646.1) shows a similar level of homology with a further brain tissue derived EST (AI589129) (TBlastN, BLAST, Altschul, Stephen F., Gish, Warren, Miller, Webb, Myers, Eugene W., and Lipman, David J. (1990). Basic local alignment search tool. J. Mol. Biol.215; 403-410.). This EST sequence does not overlap with EST

AA326679 so that the possibility remained that the partial amino acid sequence and masses listed in Table XI could be encoded by the no-overlapping region of these 2 ESTs.

Opposing PCR primers (1 & 2 from Table XII) from EST AA326679 and EST AI589129 were used in a PCR reaction (1 ml of Advantage 2 cDNA polymerase mix (Clontech) in a buffer containing 50mM KCl, 10 mM Tris-HCl, 1.5 mM MgCl2, pH8.3; 0.2mM each of dATP, dCTP, dGTP, dTTP and 10 pmoles of oligonucleotide primers. Reactions were routinely made to a final volume of 50ml and amplification carried out in a PE GeneAmpSystems 9700 PCR machine with the following cycling conditions: initial denaturation of 94 °C for 1 minute followed by 30 cycles of 94 °C for 30 seconds, 55 °C for 30 seconds and 72 °C for 2 minutes. Reaction products were resolved by standard agarose gel electrophoresis and stained with Ethidium Bromide) on 10ng of whole brain cDNA (Clontech, USA). The resulting 1.6kb fragment was purified from primers and buffers (Qiagen, UK) and sequenced using the primers given in Table XII (1,2, 3 & 4). This generated overlapping sequence for the entire product. Analysis of this DNA sequence (GCG, UK) shows a complete ORF now including the partial amino acid sequence and masses listed in Table XI. SEQ ID no.1 and Figure 2A show the DNA sequence. SEQ ID no. 2 and Figure 2B show the protein sequence of the open reading frame (ORF) seen in SEQ ID no.1, demonstrating the presence of the two peptides identified by mass spectrometry.

Table XII. Primer Sequences

Primer	Name	Sequence (5' --- 3')
1	F1	gcctaatggntcccaaactc
2	R1	gaggtgaatctgtcagtggatc
3	SF	atggaagaggctggctctgttg
4	SR	aagagatgggtacctccagagg

The DNA sequences encoding the sequences of two identified peptides are as follows:

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gag tgg gtg gcc atc gag agc gac tct gtc cag cct gtg cct
Glu Trp Val Ala Ile Glu Ser Asp Ser Val Gln Pro Val Pro
```

and

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gcc atc cat cta gac cta gaa gaa tac cgg
Ala Ile His Leu Asp Leu Glu Glu Tyr Arg
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A Blast search against High Throughput Genomic Sequencing data (http://www.ncbi.nlm.nih.gov/blast) localised the sequence from DPI 45 and DPI-213, EWVAIESDSVQPVPR, to chromosome 18 - clone RP11-231E4, map 18 (AC009704).

In a parallel study on schizophrenia, the protein corresponding to DPI 45 and DPI-213 was also found to be differentially present in a sample of CSF from a subject having Schizophrenia compared with a sample of CSF from a subject free from Schizophrenia, being decreased 1.50 fold. WO99/58660 disclosed 97 human secreted proteins. These included a sequence, identified as Gene No: 21, which corresponds to DPI 45 discussed herein. However, this disclosure did not provide any isolated protein, nor did it describe the Post-Translational Modifications characterised above, nor did it identify DPI 45 or DPI-213 as being differentially present in samples of CSF from subjects having BAD compared with a sample of CSF subjects free from BAD and in samples of CSF from subjects having Schizophrenia compared with a sample of CSF subjects free from Schizophrenia.

Expression of DPI 45 and DPI-213 mRNA in Human Tissues

We used real time quantitative RT-PCR (Heid et al., 1996; Morrison et al., 1998) to analyse the distribution of DPI 45 and DPI-213 mRNA in normal human tissues (Figure 3). The distribution of DPI 45 and DPI-213 mRNA was restricted in the body and elevated in all parts of the brain.

Predictive Analysis of DPI 45

Although SEQ ID no.1 shares 44% identity with a putative human protein derived from a conceptual translation of the cDNA CAB07646.1 (available at http://www.ncbi.nlm.nih.gov/entrez/), no function has been assigned to CAB07646.1. PSORT (Nakai, K. and Kanehisa, M., A knowledge base for predicting protein localization sites in eukaryotic cells, Genomics 14, 897-911 (1992)) analysis of SEQ

ID no.1 identifies only a signal sequence at amino acids 1-20, with proteolytic cleavage predicted between amino acids 20 and 21.

Thus the mRNA expression and protein structure analyses are consistent with this protein being secreted from brain tissues and being assayable in CSF.

5.7 Expression of DNA Encoding DPIs

The nucleotide sequence coding for a DPI, a DPI analog, a DPI-related peptide, or a fragment or other derivative of any of the foregoing, can be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for the transcription and translation of the inserted protein-coding sequence. The necessary transcriptional and translational signals can also be supplied by the native gene encoding the DPI or its flanking regions, or the native gene encoding the DPI-related polypeptide or its flanking regions. A variety of host-vector systems may be utilized in the present invention to express the protein-coding sequence. These include but are not limited to mammalian cell systems infected with virus (e.g., vaccinia virus, adenovirus, etc.); insect cell systems infected with virus (e.g., baculovirus); microorganisms such as yeast containing yeast vectors; or bacteria transformed with bacteriophage, DNA, plasmid DNA, or cosmid DNA. The expression elements of vectors vary in their strengths and specificities. Depending on the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used. In specific embodiments, a nucleotide sequence encoding a human gene (or a nucleotide sequence encoding a functionally active portion of a human DPI) is expressed. In yet another embodiment, a fragment of a DPI comprising a domain of the DPI is expressed.

Any of the methods previously described for the insertion of DNA fragments into a vector may be used to construct expression vectors containing a chimeric gene consisting of appropriate transcriptional and translational control signals and the protein coding sequences. These methods may include *in vitro* recombinant DNA and synthetic techniques and *in vivo* recombinants (genetic recombination). Expression of nucleic acid sequence encoding a DPI or fragment thereof may be regulated by a second nucleic acid sequence so that the DPI or fragment is expressed in a host transformed with the recombinant DNA molecule. For example, expression of a DPI may be controlled by any promoter or enhancer element known in the art. Promoters which may be used to control the expression of the gene encoding a DPI or a DPI-

related polypeptide include, but are not limited to, the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, et al., 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al., 1982, Nature 296:39- 42), the tetracycline (Tet) promoter (Gossen et al., 1995, Proc. Nat. Acad. Sci. USA 89:5547-5551); prokaryotic expression vectors such as the β-lactamase promoter (Villa- Kamaroff, et al., 1978, Proc. Natl. Acad. Sci. U.S.A. 75:3727-3731), or the tac promoter (DeBoer, et al., 1983, Proc. Natl. Acad. Sci. U.S.A. 80:21-25; see also "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242:74-94); plant expression vectors comprising the nopaline synthetase promoter region (Herrera-Estrella et al., Nature 303:209-213) or the cauliflower mosaic virus 35S RNA promoter (Gardner, et al., 1981, Nucl. Acids Res. 9:2871), and the promoter of the photosynthetic enzyme ribulose biphosphate carboxylase (Herrera-Estrella et al., 1984, Nature 310:115-120); promoter elements from yeast or other fungi such as the Gal 4 promoter, the ADC (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, alkaline phosphatase promoter, and the following animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: elastase I gene control region which is active in pancreatic acinar cells (Swift et al., 1984, Cell 38:639- 646; Ornitz et al., 1986, Cold Spring Harbor Symp. Quant. Biol. 50:399-409; MacDonald, 1987, Hepatology 7:425-515); insulin gene control region which is active in pancreatic beta cells (Hanahan, 1985, Nature 315:115-122), immunoglobulin gene control region which is active in lymphoid cells (Grosschedl et al., 1984, Cell 38:647-658; Adames et al., 1985, Nature 318:533-538; Alexander et al., 1987, Mol. Cell. Biol. 7:1436-1444), mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells (Leder et al., 1986, Cell 45:485-495), albumin gene control region which is active in liver (Pinkert et al., 1987, Genes and Devel. 1:268- 276), alpha-fetoprotein gene control region which is active in liver (Krumlauf et al., 1985, Mol. Cell. Biol. 5:1639-1648; Hammer et al., 1987, Science 235:53-58; alpha 1- antitrypsin gene control region which is active in the liver (Kelsey et al., 1987, Genes and Devel. 1:161-171), beta-globin gene control region which is active in myeloid cells (Mogram et al., 1985, Nature 315:338-340; Kollias et

al., 1986, Cell 46:89-94; myelin basic protein gene control region which is active in oligodendrocyte cells in the brain (Readhead et al., 1987, Cell 48:703-712); myosin light chain-2 gene control region which is active in skeletal muscle (Sani, 1985, Nature 314:283-286); neuronal-specific enolase (NSE) which is active in neuronal cells (Morelli et al., 1999, Gen. Virol. 80:571-83); brain-derived neurotrophic factor (BDNF) gene control region which is active in neuronal cells (Tabuchi et al., 1998, Biochem. Biophysic. Res. Com. 253:818- 823); glial fibrillary acidic protein (GFAP) promoter which is active in astrocytes (Gomes et al., 1999, Braz J Med Biol Res 32(5):619-631; Morelli et al., 1999, Gen. Virol. 80:571-83) and gonadotropic releasing hormone gene control region which is active in the hypothalamus (Mason et al., 1986, Science 234:1372-1378).

In a specific embodiment, a vector is used that comprises a promoter operably linked to a DPI-encoding nucleic acid, one or more origins of replication, and, optionally, one or more selectable markers (e.g., an antibiotic resistance gene).

In a specific embodiment, an expression construct is made by subcloning a DPI or a DPI-related polypeptide coding sequence into the EcoRI restriction site of each of the three pGEX vectors (Glutathione S-Transferase expression vectors; Smith and Johnson, 1988, Gene 7:31-40). This allows for the expression of the DPI product or DPI-related polypeptide from the subclone in the correct reading frame.

In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the DPI coding sequence or DPI-related polypeptide coding sequence may be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by *in vitro* or *in vivo* recombination. Insertion in a non-essential region of the viral genome (e.g., region E1 or E3) will result in a recombinant virus that is viable and capable of expressing the antibody molecule in infected hosts. (e.g., see Logan & Shenk, 1984, Proc. Natl. Acad. Sci. USA 81:355-359). Specific initiation signals may also be required for efficient translation of inserted antibody coding sequences. These signals include the ATG initiation codon and adjacent sequences. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate

transcription enhancer elements, transcription terminators, etc. (see Bittner et al., 1987, Methods in Enzymol. 153:51-544).

Expression vectors containing inserts of a gene encoding a DPI or a DPI-related polypeptide can be identified by three general approaches: (a) nucleic acid hybridization, (b) presence or absence of "marker" gene functions, and (c) expression of inserted sequences. In the first approach, the presence of a gene encoding a DPI inserted in an expression vector can be detected by nucleic acid hybridization using probes comprising sequences that are homologous to an inserted gene encoding a DPI. In the second approach, the recombinant vector/host system can be identified and selected based upon the presence or absence of certain "marker" gene functions (e.g., thymidine kinase activity, resistance to antibiotics, transformation phenotype, occlusion body formation in baculovirus, etc.) caused by the insertion of a gene encoding a DPI in the vector. For example, if the gene encoding the DPI is inserted within the marker gene sequence of the vector, recombinants containing the gene encoding the DPI insert can be identified by the absence of the marker gene function. In the third approach, recombinant expression vectors can be identified by assaying the gene product (i.e., DPI) expressed by the recombinant. Such assays can be based, for example, on the physical or functional properties of the DPI in *in vitro* assay systems, e.g., binding with anti-DPI antibody.

In addition, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Expression from certain promoters can be elevated in the presence of certain inducers; thus, expression of the genetically engineered DPI or DPI-related polypeptide may be controlled. Furthermore, different host cells have characteristic and specific mechanisms for the translational and post-translational processing and modification (e.g., glycosylation, phosphorylation of proteins). Appropriate cell lines or host systems can be chosen to ensure the desired modification and processing of the foreign protein expressed. For example, expression in a bacterial system will produce an unglycosylated product and expression in yeast will produce a glycosylated product. Eukaryotic host cells which possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product may be used. Such mammalian host cells include but are not limited to CHO, VERO, BHK, Hela, COS, MDCK, 293, 3T3, WI38, and in particular, neuronal cell lines such as, for example, SK-N-AS, SK-N-FI, SK-N-DZ human neuroblastomas

(Sugimoto et al., 1984, J. Natl. Cancer Inst. 73: 51-57), SK-N-SH human neuroblastoma (Biochim. Biophys. Acta, 1982, 704: 450-460), Daoy human cerebellar medulloblastoma (He et al., 1992, Cancer Res. 52: 1144-1148) DBTRG-05MG glioblastoma cells (Kruse et al., 1992, *In vitro* Cell. Dev. Biol. 28A: 609-614), IMR-32 human neuroblastoma (Cancer Res., 1970, 30: 2110-2118), 1321N1 human astrocytoma (Proc. Natl Acad. Sci. USA ,1977, 74: 4816), MOG-G-CCM human astrocytoma (Br. J. Cancer, 1984, 49: 269), U87MG human glioblastoma-astrocytoma (Acta Pathol. Microbiol. Scand., 1968, 74: 465-486), A172 human glioblastoma (Olopade et al., 1992, Cancer Res. 52: 2523-2529), C6 rat glioma cells (Benda et al., 1968, Science 161: 370-371), Neuro-2a mouse neuroblastoma (Proc. Natl. Acad. Sci. USA, 1970, 65: 129-136), NB41A3 mouse neuroblastoma (Proc. Natl. Acad. Sci. USA, 1962, 48: 1184-1190), SCP sheep choroid plexus (Bolin et al., 1994, J. Virol. Methods 48: 211-221), G355-5, PG-4 Cat normal astrocyte (Haapala et al., 1985, J. Virol. 53: 827-833), Mpf ferret brain (Trowbridge et al., 1982, *In vitro* 18: 952-960), and normal cell lines such as, for example, CTX TNA2 rat normal cortex brain (Radany et al., 1992, Proc. Natl. Acad. Sci. USA 89: 6467-6471) such as, for example, CRL7030 and Hs578Bst. Furthermore, different vector/host expression systems may effect processing reactions to different extents.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express the differentially expressed or pathway gene protein may be engineered. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of the foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched medium, and then are switched to a selective medium. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines. This method may advantageously be used to engineer cell lines which express the differentially expressed or pathway gene protein. Such engineered cell lines may be particularly useful in screening and evaluation of compounds that affect the endogenous activity of the differentially expressed or pathway gene protein.

A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler, et al., 1977, Cell 11:223), hypoxanthine-guanine phosphoribosyltransferase (Szybalska & Szybalski, 1962, Proc. Natl. Acad. Sci. USA 48:2026), and adenine phosphoribosyltransferase (Lowy, et al., 1980, Cell 22:817) genes can be employed in tk-, hgprt- or aprt- cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for dhfr, which confers resistance to methotrexate (Wigler, et al., 1980, Natl. Acad. Sci. USA 77:3567; O'Hare, et al., 1981, Proc. Natl. Acad. Sci. USA 78:1527); gpt, which confers resistance to mycophenolic acid (Mulligan & Berg, 1981, Proc. Natl. Acad. Sci. USA 78:2072); neo, which confers resistance to the aminoglycoside G-418 (Colberre-Garapin, et al., 1981, J. Mol. Biol. 150:1); and hygro, which confers resistance to hygromycin (Santerre, et al., 1984, Gene 30:147) genes.

In other specific embodiments, the DPI, fragment, analog, or derivative may be expressed as a fusion, or chimeric protein product (comprising the protein, fragment, analog, or derivative joined via a peptide bond to a heterologous protein sequence). For example, the polypeptides of the present invention may be fused with the constant domain of immunoglobulins (IgA, IgE, IgG, IgM), or portions thereof (CH1, CH2, CH3, or any combination thereof and portions thereof) resulting in chimeric polypeptides. Such fusion proteins may facilitate purification, increase half-life *in vivo*, and enhance the delivery of an antigen across an epithelial barrier to the immune system. An increase in the half-life *in vivo* and facilitated purification has been shown for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. See, e.g., EP 394,827; Traunecker et al., Nature, 331:84-86 (1988). Enhanced delivery of an antigen across the epithelial barrier to the immune system has been demonstrated for antigens (e.g., insulin) conjugated to an FcRn binding partner such as IgG or Fc fragments (see, e.g., PCT publications WO 96/22024 and WO 99/04813).

Nucleic acids encoding a DPI, a fragment of a DPI, a DPI-related polypeptide, or a fragment of a DPI-related polypeptide can be fused to an epitope tag (e.g., the hemagglutinin ("HA") tag or flag tag) to aid in detection and purification of the expressed polypeptide. For example, a system described by Janknecht et al. allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht et al., 1991, Proc. Natl. Acad. Sci. USA 88:8972-897).

Fusion proteins can be made by ligating the appropriate nucleic acid sequences encoding the desired amino acid sequences to each other by methods known in the art, in the proper coding frame, and expressing the chimeric product by methods commonly known in the art. Alternatively, a fusion protein may be made by protein synthetic techniques, e.g., by use of a peptide synthesizer.

Both cDNA and genomic sequences can be cloned and expressed.

5.8 Domain Structure of DPIs

Domains of some DPIs are known in the art and have been described in the scientific literature. Moreover, domains of a DPI can be identified using techniques known to those of skill in the art. For example, one or more domains of a DPI can be identified by using one or more of the following programs: ProDom, TMpred, and SAPS. ProDom compares the amino acid sequence of a polypeptide to a database of compiled domains (see, e.g., http://www.toulouse.inra.fr/prodom.html; Corpet F., Gouzy J. & Kahn D., 1999, Nucleic Acids Res., 27:263-267). TMpred predicts membrane-spanning regions of a polypeptide and their orientation. This program uses an algorithm that is based on the statistical analysis of TMbase, a database of naturally occuring transmembrane proteins (see, e.g., http://www.ch.embnet.org/software/TMPRED_form.html; Hofmann & Stoffel. (1993) "TMbase - A database of membrane spanning proteins segments." Biol. Chem. Hoppe-Seyler 347,166). The SAPS program analyzes polypeptides for statistically significant features like charge-clusters, repeats, hydrophobic regions, compositional domains (see, e.g., Brendel et al., 1992, Proc. Natl. Acad. Sci. USA 89: 2002-2006). Thus, based on the present description, the skilled artisan can identify domains of a DPI having enzymatic or binding activity, and further can identify nucleotide sequences encoding such domains. These nucleotide sequences can then be used for recombinant expression of a DPI fragment that retains the enzymatic or binding activity of the DPI.

Based on the present description, the skilled artisan can identify domains of a DPI having enzymatic or binding activity, and further can identify nucleotide sequences encoding such domains. These nucleotide sequences can then be used for recombinant expression of DPI fragments that retain the enzymatic or binding activity of the DPI.

In one embodiment, a DPI has an amino acid sequence sufficiently similar to an identified domain of a known polypeptide. As used herein, the term "sufficiently similar" refers to a first amino acid or nucleotide sequence which contains a sufficient number of identical or equivalent (e.g., with a similar side chain) amino acid residues or nucleotides to a second amino acid or nucleotide sequence such that the first and second amino acid or nucleotide sequences have or encode a common structural domain or common functional activity or both.

A DPI domain can be assessed for its function using techniques well known to those of skill in the art. For example, a domain can be assessed for its kinase activity or for its ability to bind to DNA using techniques known to the skilled artisan. Kinase activity can be assessed, for example, by measuring the ability of a polypeptide to phosphorylate a substrate. DNA binding activity can be assessed, for example, by measuring the ability of a polypeptide to bind to a DNA binding element in a electromobility shift assay. In a preferred embodiment, the function of a domain of a DPI is determined using an assay described in one or more of the references identified in Table XIII, infra.

5.9 Production of Antibodies to DPIs

According to the invention a DPI, DPI analog, DPI-related protein or a fragment or derivative of any of the foregoing may be used as an immunogen to generate antibodies which immunospecifically bind such an immunogen. Such immunogens can be isolated by any convenient means, including the methods described above. Antibodies of the invention include, but are not limited to polyclonal, monoclonal, bispecific, humanized or chimeric antibodies, single chain antibodies, Fab fragments and F(ab') fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies, and epitope-binding fragments of any of the above. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that specifically binds an antigen. The immunoglobulin molecules of the invention can be of any class (e.g., IgG, IgE, IgM, IgD and IgA) or subclass of immunoglobulin molecule.

In one embodiment, antibodies that recognize gene products of genes encoding DPIs are publicly available. For example, antibodies that recognize these DPIs and/or their isoforms include antibodies recognizing, DPI-3, DPI-5, DPI-8, DPI-

9, DPI-10, DPI-11, DPI-12, DPI-13, DPI-14, DPI-15, DPI-17, DPI-19, DPI-20, DPI-23, DPI-24, DPI-25, DPI-29, DPI-30, DPI-35, DPI-37, DPI-44, DPI-51, DPI-57, DPI-58, DPI-59, DPI-60, DPI-65, DPI-66, DPI-67, DPI-71, DPI-72, DPI-73, DPI-75, DPI-76, DPI-79, DPI-87, DPI-88, DPI-89, DPI-90, DPI-92, DPI-108, DPI-109, DPI-110, DPI-113, DPI-115, DPI-116, DPI-119, DPI-120, DPI-127, DPI-128, DPI-129, DPI-135, DPI-139, DPI-140, DPI-143, DPI-144, DPI-145, DPI-146, DPI-147, DPI-155, DPI-160, DPI-161, DPI-175, DPI-177, DPI-178, DPI-179, DPI-181, DPI-185, DPI-187, DPI-188, DPI-189, DPI-190, DPI-194, DPI-195, DPI-196, DPI-198, DPI-199, DPI-200, DPI-201, DPI-202, DPI-206, DPI-209, DPI-211, DPI-212, DPI-214, DPI-215, DPI-216, DPI-223, DPI-224, DPI-225, DPI-226, DPI-228, DPI-230, DPI-231, DPI-232, DPI-235, DPI-237, DPI-240, DPI-241, DPI-244, DPI-245, DPI-246, DPI-247, DPI-249, DPI-250, DPI-251, DPI-252, DPI-254, DPI-258, DPI-259, DPI-261, DPI-262, DPI-264, DPI-265, DPI-267, DPI-268, DPI-270, DPI-271, DPI-272, DPI-274, DPI-279, DPI-280, DPI-281, which antibodies can be purchased from commercial sources as shown in Table VII above. In another embodiment, methods known to those skilled in the art are used to produce antibodies that recognize a DPI, a DPI analog, a DPI-related polypeptide, or a derivative or fragment of any of the foregoing.

In one embodiment of the invention, antibodies to a specific domain of a DPI are produced. In a specific embodiment, hydrophilic fragments of a DPI are used as immunogens for antibody production.

In the production of antibodies, screening for the desired antibody can be accomplished by techniques known in the art, e.g. ELISA (enzyme-linked immunosorbent assay). For example, to select antibodies which recognize a specific domain of a DPI, one may assay generated hybridomas for a product which binds to a DPI fragment containing such domain. For selection of an antibody that specifically binds a first DPI homolog but which does not specifically bind to (or binds less avidly to) a second DPI homolog, one can select on the basis of positive binding to the first DPI homolog and a lack of binding to (or reduced binding to) the second DPI homolog. Similarly, for selection of an antibody that specifically binds a DPI but which does not specifically bind to (or binds less avidly to) a different isoform of the same protein (such as a different glycoform having the same core peptide as the DPI), one can select on the basis of positive binding to the DPI and a lack of binding to (or reduced binding to) the different isoform (e.g., a different glycoform). Thus, the

present invention provides an antibody (preferably a monoclonal antibody) that binds with greater affinity (preferably at least 2-fold, more preferably at least 5-fold still more preferably at least 10-fold greater affinity) to a DPI than to a different isoform or isoforms (e.g., glycoforms) of the DPI.

Polyclonal antibodies which may be used in the methods of the invention are heterogeneous populations of antibody molecules derived from the sera of immunized animals. Unfractionated immune serum can also be used. Various procedures known in the art may be used for the production of polyclonal antibodies to a DPI, a fragment of a DPI, a DPI-related polypeptide, or a fragment of a DPI-related polypeptide. In a particular embodiment, rabbit polyclonal antibodies to an epitope of a DPI or a DPI-related polypeptide can be obtained. For example, for the production of polyclonal or monoclonal antibodies, various host animals can be immunized by injection with the native or a synthetic (e.g., recombinant) version of a DPI, a fragment of a DPI, a DPI-related polypeptide, or a fragment of a DPI-related polypeptide, including but not limited to rabbits, mice, rats, etc. The Preferred Technology described herein provides isolated DPIs suitable for such immunization. If the DPI is purified by gel electrophoresis, the DPI can be used for immunization with or without prior extraction from the polyacrylamide gel. Various adjuvants may be used to enhance the immunological response, depending on the host species, including, but not limited to, complete or incomplete Freund's adjuvant, a mineral gel such as aluminum hydroxide, surface active substance such as lysolecithin, pluronic polyol, a polyanion, a peptide, an oil emulsion, keyhole limpet hemocyanin, dinitrophenol, and an adjuvant such as BCG (bacille Calmette-Guerin) or corynebacterium parvum. Additional adjuvants are also well known in the art.

For preparation of monoclonal antibodies (mAbs) directed toward a DPI, a fragment of a DPI, a DPI-related polypeptide, or a fragment of a DPI-related polypeptide, any technique which provides for the production of antibody molecules by continuous cell lines in culture may be used. For example, the hybridoma technique originally developed by Kohler and Milstein (1975, Nature 256:495-497), as well as the trioma technique, the human B-cell hybridoma technique (Kozbor et al., 1983, Immunology Today 4:72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., 1985, in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., pp. 77-96). Such antibodies may be of any immunoglobulin class including IgG, IgM, IgE, IgA, IgD and any subclass thereof.

The hybridoma producing the mAbs of the invention may be cultivated *in vitro* or *in vivo*. In an additional embodiment of the invention, monoclonal antibodies can be produced in germ-free animals utilizing known technology (PCT/US90/02545, incorporated herein by reference).

The monoclonal antibodies include but are not limited to human monoclonal antibodies and chimeric monoclonal antibodies (e.g., human-mouse chimeras). A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a human immunoglobulin constant region and a variable region derived from a murine mAb. (See, e.g., Cabilly et al., U.S. Patent No. 4,816,567; and Boss et al., U.S. Patent No. 4,816397, which are incorporated herein by reference in their entirety.) Humanized antibodies are antibody molecules from non- human species having one or more complementarily determining regions (CDRs) from the non-human species and a framework region from a human immunoglobulin molecule. (See, e.g., Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.)

Chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT Publication No. WO 87/02671; European Patent Application 184,187; European Patent Application 171,496; European Patent Application 173,494; PCT Publication No. WO 86/01533; U.S. Patent No. 4,816,567; European Patent Application 125,023; Better et al., 1988, Science 240:1041-1043; Liu et al., 1987, Proc. Natl. Acad. Sci. USA 84:3439-3443; Liu et al., 1987, J. Immunol. 139:3521-3526; Sun et al., 1987, Proc. Natl. Acad. Sci. USA 84:214-218; Nishimura et al., 1987, Canc. Res. 47:999-1005; Wood et al., 1985, Nature 314:446-449; and Shaw et al., 1988, J. Natl. Cancer Inst. 80:1553-1559; Morrison, 1985, Science 229:1202-1207; Oi et al., 1986, Bio/Techniques 4:214; U.S. Patent 5,225,539; Jones et al., 1986, Nature 321:552-525; Verhoeyan et al. (1988) Science 239:1534; and Beidler et al., 1988, J. Immunol. 141:4053-4060.

Completely human antibodies are particularly desirable for therapeutic treatment of human subjects. Such antibodies can be produced using transgenic mice which are incapable of expressing endogenous immunoglobulin heavy and light chains genes, but which can express human heavy and light chain genes. The transgenic mice are immunized in the normal fashion with a selected antigen, e.g., all or a portion of a DPI of the invention. Monoclonal antibodies directed against the

antigen can be obtained using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA, IgM and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar (1995, Int. Rev. Immunol. 13:65-93). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., U.S. Patent 5,625,126; U.S. Patent 5,633,425; U.S. Patent 5,569,825; U.S. Patent 5,661,016; and U.S. Patent 5,545,806. In addition, companies such as Abgenix, Inc. (Freemont, CA) and Genpharm (San Jose, CA) can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, e.g., a mouse antibody, is used to guide the selection of a completely human antibody recognizing the same epitope. (Jespers et al. (1994) Bio/technology 12:899-903).

The antibodies of the present invention can also be generated using various phage display methods known in the art. In phage display methods, functional antibody domains are displayed on the surface of phage particles which carry the polynucleotide sequences encoding them. In a particular, such phage can be utilized to display antigen binding domains expressed from a repertoire or combinatorial antibody library (e.g., human or murine). Phage expressing an antigen binding domain that binds the antigen of interest can be selected or identified with antigen, e.g., using labeled antigen or antigen bound or captured to a solid surface or bead. Phage used in these methods are typically filamentous phage including fd and M13 binding domains expressed from phage with Fab, Fv or disulfide stabilized Fv antibody domains recombinantly fused to either the phage gene III or gene VIII protein. Phage display methods that can be used to make the antibodies of the present invention include those disclosed in Brinkman et al., J. Immunol. Methods 182:41-50 (1995); Ames et al., J. Immunol. Methods 184:177- 186 (1995); Kettleborough et al., Eur. J. Immunol. 24:952-958 (1994); Persic et al., Gene 187 9-18 (1997); Burton et al., Advances in Immunology 57:191-280 (1994); PCT Application No.

PCT/GB91/01134; PCT Publications WO 90/02809; WO 91/10737; WO 92/01047; WO 92/18619; WO 93/11236; WO 95/15982; WO 95/20401; and U.S. Patent Nos. 5,698,426; 5,223,409; 5,403,484; 5,580,717; 5,427,908; 5,750,753; 5,821,047; 5,571,698; 5,427,908; 5,516,637; 5,780,225; 5,658,727; 5,733,743 and 5,969,108; each of which is incorporated herein by reference in its entirety.

As described in the above references, after phage selection, the antibody coding regions from the phage can be isolated and used to generate whole antibodies, including human antibodies, or any other desired antigen binding fragment, and expressed in any desired host, including mammalian cells, insect cells, plant cells, yeast, and bacteria, e.g., as described in detail below. For example, techniques to recombinantly produce Fab, Fab' and F(ab')2 fragments can also be employed using methods known in the art such as those disclosed in PCT publication WO 92/22324; Mullinax et al., BioTechniques 12(6):864-869 (1992); and Sawai et al., AJRI 34:26-34 (1995); and Better et al., Science 240:1041-1043 (1988) (said references incorporated by reference in their entireties).

Examples of techniques which can be used to produce single-chain Fvs and antibodies include those described in U.S. Patents 4,946,778 and 5,258,498; Huston et al., Methods in Enzymology 203:46-88 (1991); Shu et al., PNAS 90:7995-7999 (1993); and Skerra et al., Science 240:1038-1040 (1988).

The invention further provides for the use of bispecific antibodies, which can be made by methods known in the art. Traditional production of full length bispecific antibodies is based on the coexpression of two immunoglobulin heavy chain-light chain pairs, where the two chains have different specificities (Milstein et al., 1983, Nature 305:537-539). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of 10 different antibody molecules, of which only one has the correct bispecific structure. Purification of the correct molecule, which is usually done by affinity chromatography steps, is rather cumbersome, and the product yields are low. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., 1991, EMBO J. 10:3655-3659 .

According to a different and more preferred approach, antibody variable domains with the desired binding specificities (antibody-antigen combining sites) are fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy chain constant domain, comprising at least part of the

hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light chain binding, present in at least one of the fusions. DNAs encoding the immunoglobulin heavy chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. This provides for great flexibility in adjusting the mutual proportions of the three polypeptide fragments in embodiments when unequal ratios of the three polypeptide chains used in the construction provide the optimum yields. It is, however, possible to insert the coding sequences for two or all three polypeptide chains in one expression vector when the expression of at least two polypeptide chains in equal ratios results in high yields or when the ratios are of no particular significance.

In a preferred embodiment of this approach, the bispecific antibodies are composed of a hybrid immunoglobulin heavy chain with a first binding specificity in one arm, and a hybrid immunoglobulin heavy chain-light chain pair (providing a second binding specificity) in the other arm. It was found that this asymmetric structure facilitates the separation of the desired bispecific compound from unwanted immunoglobulin chain combinations, as the presence of an immunoglobulin light chain in only one half of the bispecific molecule provides for a facile way of separation. This approach is disclosed in WO 94/04690 published March 3,1994. For further details for generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology,1986, 121:210.

The invention provides functionally active fragments, derivatives or analogs of the anti-DPI immunoglobulin molecules. Functionally active means that the fragment, derivative or analog is able to elicit anti-anti-idiotype antibodies (i.e., tertiary antibodies) that recognize the same antigen that is recognized by the antibody from which the fragment, derivative or analog is derived. Specifically, in a preferred embodiment the antigenicity of the idiotype of the immunoglobulin molecule may be enhanced by deletion of framework and CDR sequences that are C-terminal to the CDR sequence that specifically recognizes the antigen. To determine which CDR sequences bind the antigen, synthetic peptides containing the CDR sequences can be used in binding assays with the antigen by any binding assay method known in the a

The present invention provides antibody fragments such as, but not limited to, F(ab')2 fragments and Fab fragments. Antibody fragments which recognize specific epitopes may be generated by known techniques. F(ab')2 fragments consist of the

variable region, the light chain constant region and the CH1 domain of the heavy chain and are generated by pepsin digestion of the antibody molecule. Fab fragments are generated by reducing the disulfide bridges of the F(ab')2 fragments. The invention also provides heavy chain and light chain dimers of the antibodies of the invention, or any minimal fragment thereof such as Fvs or single chain antibodies (SCAs) (e.g., as described in U.S. Patent 4,946,778; Bird, 1988, Science 242:423-42; Huston et al., 1988, Proc. Natl. Acad. Sci. USA 85:5879-5883; and Ward et al., 1989, Nature 334:544-54), or any other molecule with the same specificity as the antibody of the invention. Single chain antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain polypeptide. Techniques for the assembly of functional Fv fragments in E. coli may be used (Skerra et al., 1988, Science 242:1038-1041).

In other embodiments, the invention provides fusion proteins of the immunoglobulins of the invention (or functionally active fragments thereof), for example in which the immunoglobulin is fused via a covalent bond (e.g., a peptide bond), at either the N-terminus or the C-terminus to an amino acid sequence of another protein (or portion thereof, preferably at least 10, 20 or 50 amino acid portion of the protein) that is not the immunoglobulin. Preferably the immunoglobulin, or fragment thereof, is covalently linked to the other protein at the N-terminus of the constant domain. As stated above, such fusion proteins may facilitate purification, increase half-life *in vivo*, and enhance the delivery of an antigen across an epithelial barrier to the immune system.

The immunoglobulins of the invention include analogs and derivatives that are either modified, i.e, by the covalent attachment of any type of molecule as long as such covalent attachment that does not impair immunospecific binding. For example, but not by way of limitation, the derivatives and analogs of the immunoglobulins include those that have been further modified, e.g., by glycosylation, acetylation, pegylation, phosphylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein, etc. Any of numerous chemical modifications may be carried out by known techniques, including, but not limited to specific chemical cleavage, acetylation, formylation, etc. Additionally, the analog or derivative may contain one or more non-classical amino acids.

The foregoing antibodies can be used in methods known in the art relating to the localization and activity of the DPIs of the invention, e.g., for imaging these proteins, measuring levels thereof in appropriate physiological samples, in diagnostic methods, etc.

5.10 Expression Of Antibodies

The antibodies of the invention can be produced by any method known in the art for the synthesis of antibodies, in particular, by chemical synthesis or by recombinant expression, and are preferably produced by recombinant expression techniques.

Recombinant expression of antibodies, or fragments, derivatives or analogs thereof, requires construction of a nucleic acid that encodes the antibody. If the nucleotide sequence of the antibody is known, a nucleic acid encoding the antibody may be assembled from chemically synthesized oligonucleotides (e.g., as described in Kutmeier et al., 1994, BioTechniques 17:242), which, briefly, involves the synthesis of overlapping oligonucleotides containing portions of the sequence encoding antibody, annealing and ligation of those oligonucleotides, and then amplification of the ligated oligonucleotides by PCR.

Alternatively, the nucleic acid encoding the antibody may be obtained by cloning the antibody. If a clone containing the nucleic acid encoding the particular antibody is not available, but the sequence of the antibody molecule is known, a nucleic acid encoding the antibody may be obtained from a suitable source (e.g., an antibody cDNA library, or cDNA library generated from any tissue or cells expressing the antibody) by PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of the sequence or by cloning using an oligonucleotide probe specific for the particular gene sequence.

If an antibody molecule that specifically recognizes a particular antigen is not available (or a source for a cDNA library for cloning a nucleic acid encoding such an antibody), antibodies specific for a particular antigen may be generated by any method known in the art, for example, by immunizing an animal, such as a rabbit, to generate polyclonal antibodies or, more preferably, by generating monoclonal antibodies. Alternatively, a clone encoding at least the Fab portion of the antibody may be obtained by screening Fab expression libraries (e.g., as described in Huse et al., 1989, Science 246:1275-1281) for clones of Fab fragments that bind the specific

antigen or by screening antibody libraries (See, e.g., Clackson et al., 1991, Nature 352:624; Hane et al., 1997 Proc. Natl. Acad. Sci. USA 94:4937).

Once a nucleic acid encoding at least the variable domain of the antibody molecule is obtained, it may be introduced into a vector containing the nucleotide sequence encoding the constant region of the antibody molecule (see, e.g., PCT Publication WO 86/05807; PCT Publication WO 89/01036; and U.S. Patent No. 5,122,464). Vectors containing the complete light or heavy chain for co-expression with the nucleic acid to allow the expression of a complete antibody molecule are also available. Then, the nucleic acid encoding the antibody can be used to introduce the nucleotide substitution(s) or deletion(s) necessary to substitute (or delete) the one or more variable region cysteine residues participating in an intrachain disulfide bond with an amino acid residue that does not contain a sulfhydyl group. Such modifications can be carried out by any method known in the art for the introduction of specific mutations or deletions in a nucleotide sequence, for example, but not limited to, chemical mutagenesis, *in vitro* site directed mutagenesis (Hutchinson et al., 1978, J. Biol. Chem. 253:6551), PCT based methods, etc.

In addition, techniques developed for the production of "chimeric antibodies" (Morrison et al., 1984, Proc. Natl. Acad. Sci. 81:851-855; Neuberger et al., 1984, Nature 312:604-608; Takeda et al., 1985, Nature 314:452-454) by splicing genes from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity can be used. As described supra, a chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human antibody constant region, e.g., humanized antibodies.

Once a nucleic acid encoding an antibody molecule of the invention has been obtained, the vector for the production of the antibody molecule may be produced by recombinant DNA technology using techniques well known in the art. Thus, methods for preparing the protein of the invention by expressing nucleic acid containing the antibody molecule sequences are described herein. Methods which are well known to those skilled in the art can be used to construct expression vectors containing an antibody molecule coding sequences and appropriate transcriptional and translational control signals. These methods include, for example, *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. See, for

example, the techniques described in Sambrook et al. (1990, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY) and Ausubel et al. (eds., 1998, Current Protocols in Molecular Biology, John Wiley & Sons, NY).

The expression vector is transferred to a host cell by conventional techniques and the transfected cells are then cultured by conventional techniques to produce an antibody of the invention.

The host cells used to express a recombinant antibody of the invention may be either bacterial cells such as Escherichia coli, or, preferably, eukaryotic cells, especially for the expression of whole recombinant antibody molecule. In particular, mammalian cells such as Chinese hamster ovary cells (CHO), in conjunction with a vector such as the major intermediate early gene promoter element from human cytomegalovirus is an effective expression system for antibodies (Foecking et al., 1986, Gene 45:101; Cockett et al., 1990, Bio/Technology 8:2).

A variety of host-expression vector systems may be utilized to express an antibody molecule of the invention. Such host-expression systems represent vehicles by which the coding sequences of interest may be produced and subsequently purified, but also represent cells which may, when transformed or transfected with the appropriate nucleotide coding sequences, express the antibody molecule of the invention in situ. These include but are not limited to microorganisms such as bacteria (e.g., E. coli, B. subtilis) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing antibody coding sequences; yeast (e.g., Saccharomyces, Pichia) transformed with recombinant yeast expression vectors containing antibody coding sequences; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing the antibody coding sequences; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing antibody coding sequences; or mammalian cell systems (e.g., COS, CHO, BHK, 293, 3T3 cells) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter).

In bacterial systems, a number of expression vectors may be advantageously selected depending upon the use intended for the antibody molecule being expressed. For example, when a large quantity of such a protein is to be produced, for the generation of pharmaceutical compositions comprising an antibody molecule, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include, but are not limited, to the E. coli expression vector pUR278 (Ruther et al., 1983, EMBO J. 2:1791), in which the antibody coding sequence may be ligated individually into the vector in frame with the lac Z coding region so that a fusion protein is produced; pIN vectors (Inouye & Inouye, 1985, Nucleic Acids Res. 13:3101-3109; Van Heeke & Schuster, 1989, J. Biol. Chem. 24:5503-5509); and the like. pGEX vectors may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption and binding to a matrix glutathione-agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST moiety.

In an insect system, Autographa californica nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in Spodoptera frugiperda cells. The antibody coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter). In mammalian host cells, a number of viral-based expression systems (e.g., an adenovirus expression system) may be utilized.

As discussed above, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein.

For long-term, high-yield production of recombinant antibodies, stable expression is preferred. For example, cells lines that stably express an antibody of interest can be produced by transfecting the cells with an expression vector comprising the nucleotide sequence of the antibody and the nucleotide sequence of a selectable (e.g., neomycin or hygromycin), and selecting for expression of the selectable marker. Such engineered cell lines may be particularly useful in screening

and evaluation of compounds that interact directly or indirectly with the antibody molecule.

The expression levels of the antibody molecule can be increased by vector amplification (for a review, see Bebbington and Hentschel, The use of vectors based on gene amplification for the expression of cloned genes in mammalian cells in DNA cloning, Vol.3. (Academic Press, New York, 1987)). When a marker in the vector system expressing antibody is amplifiable, increase in the level of inhibitor present in culture of host cell will increase the number of copies of the marker gene. Since the amplified region is associated with the antibody gene, production of the antibody will also increase (Crouse et al., 1983, Mol. Cell. Biol. 3:257).

The host cell may be co-transfected with two expression vectors of the invention, the first vector encoding a heavy chain derived polypeptide and the second vector encoding a light chain derived polypeptide. The two vectors may contain identical selectable markers which enable equal expression of heavy and light chain polypeptides. Alternatively, a single vector may be used which encodes both heavy and light chain polypeptides. In such situations, the light chain should be placed before the heavy chain to avoid an excess of toxic free heavy chain (Proudfoot, 1986, Nature 322:52; Kohler, 1980, Proc. Natl. Acad. Sci. USA 77:2197). The coding sequences for the heavy and light chains may comprise cDNA or genomic DNA.

Once the antibody molecule of the invention has been recombinantly expressed, it may be purified by any method known in the art for purification of an antibody molecule, for example, by chromatography (e.g., ion exchange chromatography, affinity chromatography such as with protein A or specific antigen, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins.

Alternatively, any fusion protein may be readily purified by utilizing an antibody specific for the fusion protein being expressed. For example, a system described by Janknecht et al. allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht et al., 1991, Proc. Natl. Acad. Sci. USA 88:8972-897). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the open reading frame of the gene is translationally fused to an amino-terminal tag consisting of six histidine residues. The tag serves as a matrix binding domain for the fusion protein. Extracts from cells infected with recombinant vaccinia virus are loaded onto Ni2+ nitriloacetic acid-agarose columns

and histidine-tagged proteins are selectively eluted with imidazole-containing buffers.

5.11 Conjugated Antibodies

In a preferred embodiment, anti-DPI antibodies or fragments thereof are conjugated to a diagnostic or therapeutic moiety. The antibodies can be used for diagnosis or to determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, radioactive nuclides, positron emitting metals (for use in positron emission tomography), and nonradioactive paramagnetic metal ions. See generally U.S. Patent No. 4,741,900 for metal ions which can be conjugated to antibodies for use as diagnostics according to the present invention. Suitable enzymes include horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; suitable prosthetic groups include streptavidin, avidin and biotin; suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride and phycoerythrin; suitable luminescent materials include luminol; suitable bioluminescent materials include luciferase, luciferin, and aequorin; and suitable radioactive nuclides include 125I, 131I, 111In and 99Tc.

Anti-DPI antibodies or fragments thereof can be conjugated to a therapeutic agent or drug moiety to modify a given biological response. The therapeutic agent or drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin; a protein such as tumor necrosis factor, α-interferon, β-interferon, nerve growth factor, platelet derived growth factor, tissue plasminogen activator, a thrombotic agent or an anti-angiogenic agent, e.g., angiostatin or endostatin; or, a biological response modifier such as a lymphokine, interleukin-1 (IL-1), interleukin-2 (IL-2), interleukin-6 (IL-6), granulocyte macrophage colony stimulating factor (GM-CSF), granulocyte colony stimulating factor (G-CSF), nerve growth factor (NGF) or other growth factor.

Techniques for conjugating such therapeutic moiety to antibodies are well known, see, e.g., Arnon et al., "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in Monoclonal Antibodies And Cancer Therapy, Reisfeld

et al. (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom et al., "Antibodies For Drug Delivery", in Controlled Drug Delivery (2nd Ed.), Robinson et al. (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in Monoclonal Antibodies '84: Biological And Clinical Applications, Pinchera et al. (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in Monoclonal Antibodies For Cancer Detection And Therapy, Baldwin et al. (eds.), pp. 303-16 (Academic Press 1985), and Thorpe et al., "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", Immunol. Rev., 62:119-58 (1982).

Alternatively, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate as described by Segal in U.S. Patent No. 4,676,980.

An antibody with or without a therapeutic moiety conjugated to it can be used as a therapeutic that is administered alone or in combination with cytotoxic factor(s) and/or cytokine(s).

5.12 Diagnosis of Unipolar Depression or BAD

In accordance with the present invention, test samples of cerebrospinal fluid (CSF), serum, plasma or urine obtained from a subject suspected of having or known to have BAD can be used for diagnosis or monitoring. In one embodiment, a decreased abundance of one or more DFs or DPIs (or any combination of them) in a test sample relative to a control sample (from a subject or subjects free from BAD) or a previously determined reference range indicates the presence of BAD; DFs and DPIs suitable for this purpose are identified in Tables I and IV, respectively, as described in detail above. In another embodiment of the invention, an increased abundance of one or more DFs or DPIs (or any combination of them) in a test sample compared to a control sample or a previously determined reference range indicates the presence of BAD; DFs and DPIs suitable for this purpose are identified in Tables II and VI, respectively, as described in detail above. In another embodiment, the relative abundance of one or more DFs or DPIs (or any combination of them) in a test sample compared to a control sample or a previously determined reference range indicates a subtype of BAD (e.g., familial or sporadic BAD). In yet another embodiment, the relative abundance of one or more DFs or DPIs (or any combination of them) in a test sample relative to a control sample or a previously determined

reference range indicates the degree or severity of BAD. In any of the aforesaid methods, detection of one or more DPIs described herein may optionally be combined with detection of one or more additional biomarkers for BAD. Any suitable method in the art can be employed to measure the level of DFs and DPIs, including but not limited to the Preferred Technology described herein, kinase assays, immunoassays to detect and/or visualize the DPI (e.g., Western blot, immunoprecipitation followed by sodium dodecyl sulfate polyacrylamide gel electrophoresis, immunocytochemistry, etc.). In cases where a DPI has a known function, an assay for that function may be used to measure DPI expression. In a further embodiment, a decreased abundance of mRNA encoding one or more DPIs identified in Table IV (or any combination of them) in a test sample relative to a control sample or a previously determined reference range indicates the presence of BAD. In yet a further embodiment, an increased abundance of mRNA encoding one or more DPIs identified in Table V (or any combination of them) in a test sample relative to a control sample or previously determined reference range indicates the presence of BAD. Any suitable hybridization assay can be used to detect DPI expression by detecting and/or visualizing mRNA encoding the DPI (e.g., Northern assays, dot blots, in situ hybridization, etc.).

In another embodiment of the invention, labeled antibodies, derivatives and analogs thereof, which specifically bind to a DPI can be used for diagnostic purposes to detect, diagnose, or monitor BAD. Preferably, BAD is detected in an animal, more preferably in a mammal and most preferably in a human.

5.13 Screening Assays

The invention provides methods for identifying agents (e.g., candidate compounds or test compounds) that bind to a DPI or have a stimulatory or inhibitory effect on the expression or activity of a DPI. The invention also provides methods of identifying agents, candidate compounds or test compounds that bind to a DPI-related polypeptide or a DPI fusion protein or have a stimulatory or inhibitory effect on the expression or activity of a DPI-related polypeptide or a DPI fusion protein. Examples of agents, candidate compounds or test compounds include, but are not limited to, nucleic acids (e.g., DNA and RNA), carbohydrates, lipids, proteins, peptides, peptidomimetics, small molecules and other drugs. Agents can be obtained using any of the numerous approaches in combinatorial library methods known in the art,

including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, 1997, Anticancer Drug Des. 12:145; U.S. Patent No. 5,738,996; and U.S. Patent No.5,807,683, each of which is incorporated herein in its entirety by reference).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt et al., 1993, Proc. Natl. Acad. Sci. USA 90:6909; Erb et al., 1994, Proc. Natl. Acad. Sci. USA 91:11422; Zuckermann et al., 1994, J. Med. Chem. 37:2678; Cho et al., 1993, Science 261:1303; Carrell et al., 1994, Angew. Chem. Int. Ed. Engl. 33:2059; Carell et al., 1994, Angew. Chem. Int. Ed. Engl. 33:2061; and Gallop et al., 1994, J. Med. Chem. 37:1233, each of which is incorporated herein in its entirety by reference.

Libraries of compounds may be presented, e.g., presented in solution (e.g., Houghten, 1992, Bio/Techniques 13:412-421), or on beads (Lam, 1991, Nature 354:82- 84), chips (Fodor, 1993, Nature 364:555-556), bacteria (U.S. Patent No. 5,223,409), spores (Patent Nos. 5,571,698; 5,403,484; and 5,223,409), plasmids (Cull et al., 1992, Proc. Natl. Acad. Sci. USA 89:1865-1869) or phage (Scott and Smith, 1990, Science 249:386-390; Devlin, 1990, Science 249:404-406; Cwirla et al., 1990, Proc. Natl. Acad. Sci. USA 87:6378-6382; and Felici, 1991, J. Mol. Biol. 222:301-310), each of which is incorporated herein in its entirety by reference.

In one embodiment, agents that interact with (i.e., bind to) a DPI, a DPI fragment (e.g. a functionally active fragment), a DPI-related polypeptide, a fragment of a DPI-related polypeptide, or a DPI fusion protein are identified in a cell-based assay system. In accordance with this embodiment, cells expressing a DPI, a fragment of a DPI, a DPI-related polypeptide, a fragment of a DPI-related polypeptide, or a DPI fusion protein are contacted with a candidate compound or a control compound and the ability of the candidate compound to interact with the DPI is determined. If desired, this assay may be used to screen a plurality (e.g. a library) of candidate compounds. The cell, for example, can be of prokaryotic origin (e.g., E. coli) or eukaryotic origin (e.g., yeast or mammalian). Further, the cells can express the DPI, fragment of the DPI, DPI- related polypeptide, a fragment of the DPI-related

polypeptide, or a DPI fusion protein endogenously or be genetically engineered to express the DPI, fragment of the DPI, DPI-related polypeptide, a fragment of the DPI-related polypeptide, or a DPI fusion protein. In certain instances, the DPI, fragment of the DPI, DPI-related polypeptide, a fragment of the DPI-related polypeptide, or a DPI fusion protein or the candidate compound is labeled, for example with a radioactive label (such as ^{32}P, ^{35}S or ^{125}I) or a fluorescent label (such as fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, o-phthaldehyde or fluorescamine) to enable detection of an interaction between a DPI and a candidate compound. The ability of the candidate compound to interact directly or indirectly with a DPI, a fragment of a DPI, a DPI-related polypeptide, a fragment of a DPI-related polypeptide, or a DPI fusion protein can be determined by methods known to those of skill in the art. For example, the interaction between a candidate compound and a DPI, a fragment of a DPI, a DPI-related polypeptide, a fragment of a DPI-related polypeptide, or a DPI fusion protein can be determined by flow cytometry, a scintillation assay, immunoprecipitation or western blot analysis.

In another embodiment, agents that interact with (i.e., bind to) a DPI, a DPI fragment (e.g., a functionally active fragment) a DPI-related polypeptide, a fragment of a DPI-related polypeptide, or a DPI fusion protein are identified in a cell-free assay system. In accordance with this embodiment, a native or recombinant DPI or fragment thereof, or a native or recombinant DPI-related polypeptide or fragment thereof, or a DPI-fusion protein or fragment thereof, is contacted with a candidate compound or a control compound and the ability of the candidate compound to interact with the DPI or DPI-related polypeptide, or DPI fusion protein is determined. If desired, this assay may be used to screen a plurality (e.g. a library) of candidate compounds. Preferably, the DPI, DPI fragment, DPI-related polypeptide, a fragment of a DPI-related polypeptide, or a DPI-fusion protein is first immobilized, by, for example, contacting the DPI, DPI fragment, DPI-related polypeptide, a fragment of a DPI-related polypeptide, or a DPI fusion protein with an immobilized antibody which specifically recognizes and binds it, or by contacting a purified preparation of the DPI, DPI fragment, DPI-related polypeptide, fragment of a DPI-related polypeptide, or a DPI fusion protein with a surface designed to bind proteins. The DPI, DPI fragment, DPI-related polypeptide, a fragment of a DPI-related polypeptide, or a DPI fusion protein may be partially or completely purified (e.g., partially or completely

free of other polypeptides) or part of a cell lysate. Further, the DPI, DPI fragment, DPI-related polypeptide, a fragment of a DPI-related polypeptide may be a fusion protein comprising the DPI or a biologically active portion thereof, or DPI-related polypeptide and a domain such as glutathionine-S- transferase. Alternatively, the DPI, DPI fragment, DPI-related polypeptide, fragment of a DPI-related polypeptide or DPI fusion protein can be biotinylated using techniques well known to those of skill in the art (e.g., biotinylation kit, Pierce Chemicals; Rockford, IL). The ability of the candidate compound to interact with a DPI, DPI fragment, DPI-related polypeptide, a fragment of a DPI-related polypeptide, or a DPI fusion protein can be can be determined by methods known to those of skill in the art.

In another embodiment, a cell-based assay system is used to identify agents that bind to or modulate the activity of a protein, such as an enzyme, or a biologically active portion thereof, which is responsible for the production or degradation of a DPI or is responsible for the post- translational modification of a DPI. In a primary screen, a plurality (e.g., a library) of compounds are contacted with cells that naturally or recombinantly express: (i) a DPI, an isoform of a DPI, a DPI homolog a DPI-related polypeptide, a DPI fusion protein, or a biologically active fragment of any of the foregoing; and (ii) a protein that is responsible for processing of the DPI, DPI isoform, DPI homolog, DPI-related polypeptide, DPI fusion protein, or fragment in order to identify compounds that modulate the production, degradation, or post-translational modification of the DPI, DPI isoform, DPI homolog, DPI-related polypeptide, DPI fusion protein or fragment. If desired, compounds identified in the primary screen can then be assayed in a secondary screen against cells naturally or recombinantly expressing the specific DPI of interest. The ability of the candidate compound to modulate the production, degradation or post-translational modification of a DPI, isoform, homolog, DPI-related polypeptide, or DPI fusion protein can be determined by methods known to those of skill in the art, including without limitation, flow cytometry, a scintillation assay, immunoprecipitation and western blot analysis.

In another embodiment, agents that competitively interact with (i.e., bind to) a DPI, DPI fragment, DPI-related polypeptide, a fragment of a DPI-related polypeptide, or a DPI fusion protein are identified in a competitive binding assay. In accordance with this embodiment, cells expressing a DPI, DPI fragment, DPI-related polypeptide, a fragment of a DPI-related polypeptide, or a DPI fusion protein are contacted with a candidate compound and a compound known to interact with the DPI, DPI fragment,

DPI-related polypeptide, a fragment of a DPI-related polypeptide or a DPI fusion protein; the ability of the candidate compound to competitively interact with the DPI, DPI fragment, DPI-related polypeptide, fragment of a DPI-related polypeptide, or a DPI fusion protein is then determined. Alternatively, agents that competitively interact with (i.e., bind to) a DPI, DPI fragment, DPI-related polypeptide or fragment of a DPI-related polypeptide are identified in a cell-free assay system by contacting a DPI, DPI fragment, DPI-related polypeptide, fragment of a DPI-related polypeptide, or a DPI fusion protein with a candidate compound and a compound known to interact with the DPI, DPI- related polypeptide or DPI fusion protein. As stated above, the ability of the candidate compound to interact with a DPI, DPI fragment, DPI-related polypeptide, a fragment of a DPI-related polypeptide, or a DPI fusion protein can be determined by methods known to those of skill in the art. These assays, whether cell-based or cell-free, can be used to screen a plurality (e.g., a library) of candidate compounds.

In another embodiment, agents that modulate (i.e., upregulate or downregulate) the expression of a DPI, or a DPI-related polypeptide are identified by contacting cells (e.g., cells of prokaryotic origin or eukaryotic origin) expressing the DPI, or DPI-related polypeptide with a candidate compound or a control compound (e.g., phosphate buffered saline (PBS)) and determining the expression of the DPI, DPI-related polypeptide, or DPI fusion protein, mRNA encoding the DPI, or mRNA encoding the DPI-related polypeptide. The level of expression of a selected DPI, DPI-related polypeptide, mRNA encoding the DPI, or mRNA encoding the DPI-related polypeptide in the presence of the candidate compound is compared to the level of expression of the DPI, DPI-related polypeptide, mRNA encoding the DPI, or mRNA encoding the DPI- related polypeptide in the absence of the candidate compound (e.g., in the presence of a control compound). The candidate compound can then be identified as a modulator of the expression of the DPI, or a DPI-related polypeptide based on this comparison. For example, when expression of the DPI or mRNA is significantly greater in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of expression of the DPI or mRNA. Alternatively, when expression of the DPI or mRNA is significantly less in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of the expression of the DPI or mRNA. The level of expression of a DPI or the mRNA that encodes it can be determined by

methods known to those of skill in the art. For example, mRNA expression can be assessed by Northern blot analysis or RT-PCR, and protein levels can be assessed by western blot analysis.

In another embodiment, agents that modulate the activity of a DPI, or a DPI-related polypeptide are identified by contacting a preparation containing the DPI or DPI- related polypeptide, or cells (e.g., prokaryotic or eukaryotic cells) expressing the DPI or DPI-related polypeptide with a test compound or a control compound and determining the ability of the test compound to modulate (e.g., stimulate or inhibit) the activity of the DPI or DPI-related polypeptide. The activity of a DPI or a DPI-related polypeptide can be assessed by detecting induction of a cellular signal transduction pathway of the DPI or DPI-related polypeptide (e.g. , intracellular Ca2+, diacylglycerol, IP3, etc.), detecting catalytic or enzymatic activity of the target on a suitable substrate, detecting the induction of a reporter gene (e.g., a regulatory element that is responsive to a DPI or a DPI-related polypeptide and is operably linked to a nucleic acid encoding a detectable marker, e.g., luciferase), or detecting a cellular response, for example, cellular differentiation, or cell proliferation. Based on the present description, techniques known to those of skill in the art can be used for measuring these activities (see, e.g., U.S. Patent No. 5,401,639, which is incorporated herein by reference). The candidate compound can then be identified as a modulator of the activity of a DPI or DPI-related polypeptide by comparing the effects of the candidate compound to the control compound. Suitable control compounds include phosphate buffered saline (PBS) and normal saline (NS).

In another embodiment, agents that modulate (i.e., upregulate or downregulate) the expression, activity or both the expression and activity of a DPI or DPI-related polypeptide are identified in an animal model. Examples of suitable animals include, but are not limited to, mice, rats, rabbits, monkeys, guinea pigs, dogs and cats. Preferably, the animal used represent a model of BAD (a number of animal models for psychiatric disorders have had significant value in the search for new treatments and in the study of mechanisms. Most notably, the Porsolt forced swim test model of depression is frequently used in both these contexts (Kirby and Lucki, 1997; Rossetti et al., 1993). The two major clinical states observed in bipolar disorder (depression and mania) have also been successfully modeled (Cappeliez and Moore Prog Neuropsychopharmacol Biol Psychiatry 1990 14, 347-58). Psychostimulant treatment can produce a range of behaviors similar to that of mania including

hyperactivity, heightened sensory awareness, and alertness, and for this reason has become a very useful model for mania which exhibits (to some extent) face, construct and predictive validity. Another model that has been utilized for the development of bipolar illness is behavioral sensitization. In this model, the repeated administration of many psychostimulant drugs leads to a gradual increase or sensitization of the drug-induced behavioral; this model also has considerable construct and face validity for mania (Koob et al. Pharmacol Biochem Behav 1997 57, 513-21)). In accordance with this embodiment, the test compound or a control compound is administered (e.g., orally, rectally or parenterally such as intraperitoneally or intravenously) to a suitable animal and the effect on the expression, activity or both expression and activity of the DPI is determined. In accordance with this embodiment, the test compound or a control compound is administered (e.g., orally, rectally or parenterally such as intraperitoneally or intravenously) to a suitable animal and the effect on the expression, activity or both expression and activity or both expression and activity of the DPI or DPI-related polypeptide is determined. Changes in the expression of a DPI or DPI-related polypeptide can be assessed by the methods outlined above.

In yet another embodiment, a DPI or DPI-related polypeptide is used as a "bait protein" in a two-hybrid assay or three hybrid assay to identify other proteins that bind to or interact with a DPI or DPI-related polypeptide (see, e.g., U.S. Patent No. 5,283,317; Zervos et al. (1993) Cell 72:223-232; Madura et al. (1993) J. Biol. Chem. 268:12046-12054; Bartel et al. (1993) Bio/Techniques 14:920-924; Iwabuchi et al. (1993) Oncogene 8:1693-1696; and PCT Publication No. WO 94/10300). As those skilled in the art will appreciate, such binding proteins are also likely to be involved in the propagation of signals by the DPIs of the invention as, for example, upstream or downstream elements of a signaling pathway involving the DPIs of the invention.

Table XIII enumerates scientific publications describing suitable assays for detecting or quantifying enzymatic or binding activity of a DPI, a DPI analog, a DPI-related polypeptide, or a fragment of any of the foregoing. Each such reference is hereby incorporated in its entirety. In a preferred embodiment, an assay referenced in Table XIII is used in the screens and assays described herein, for example to screen for or identify a compound that modulates the activity of (or that modulates both the expression and activity of) a DPI, DPI analog, or DPI-related polypeptide, a fragment of any of the foregoing or a DPI fusion protein.

Table XIII

DPI	References
DPI-72, DPI-108, DPI-110	Structural Biology, 2000, 7:312-321 J. Am. Chem. Soc.,2000, 122:2178-2192
DPI-8, DPI-19, DPI-33	Clin. Chem., 1993, Feb 39(2):309-312 J. Immunol. Methods, 1987, Aug 102(1):7-14
DPI-67	J. Clin. Lab Immunol., 1986, Dec 21(4):201-207
DPI-95	Neuroendocrinology, 1992, Mar 55(3):308-16
DPI-54	J. Chromatogr., 1991, Jul 567(2):369-380. Clin. Chem., 1989, Apr 35(4):582-586.
DPI-44	J Chromatogr., 1987, Dec 18, 411:498-501 Eisei Shikenjo Hokoku, 1972, 90:89-92 Analyst, 1990, Aug 115(8):1143-4
DPI-75	Biochem. J., 1997, Mar 322(Pt 2):455-460 Biochem. Soc. Trans., 1997, Nov 25:4 S591 Biochim. Biophys. Acta, 1986, Oct, 888(3):325-331 http://www.promega.com

This invention further provides novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

5.14 Therapeutic Uses of DPIs

The invention provides for treatment or prevention of various diseases and disorders by administration of a therapeutic compound. Such compounds include but are not limited to: DPIs, DPI analogs, DPI-related polypeptides and derivatives (including fragments) thereof; antibodies to the foregoing; nucleic acids encoding DPIs, DPI analogs, DPI-related polypeptides and fragments thereof; antisense nucleic acids to a gene encoding a DPI or DPI-related polypeptide; and modulator (e.g., agonists and antagonists) of a gene encoding a DPI or DPI-related polypeptide. An important feature of the present invention is the identification of genes encoding DPIs involved in BAD. BAD can be treated (e.g. to ameliorate symptoms or to retard onset or progression) or prevented by administration of a therapeutic compound that

promotes function or expression of one or more DPIs that are decreased in the CSF of BAD subjects having BAD, or by administration of a therapeutic compound that reduces function or expression of one or more DPIs that are increased in the CSF of subjects having BAD.

In one embodiment, one or more antibodies each specifically binding to a DPI are administered alone or in combination with one or more additional therapeutic compounds or treatments. Examples of such treatments include mood stabilizers: lithium, divalproex, carbamazepine, lamotrigine; antidepressants: tricyclic antidepressants (eg. Desipramine, chlorimipramine, nortriptyline), selective serotonin reuptake inhibitors (SSRIs including fluoxetine (Prozac), sertraltrine (Zoloft), paroxitene (Paxil), fluvoxamine (Luvox), and citalopram (Celexa)), MAOIs, bupropion (Wellbutrin), venlafaxine (Effexor), and mirtazapine (Remeron); and atypical antipsychotic agents: Clozapine, Olanzapine, Risperidone.

Preferably, a biological product such as an antibody is allogeneic to the subject to which it is administered. In a preferred embodiment, a human DPI or a human DPI- related polypeptide, a nucleotide sequence encoding a human DPI or a human DPI- related polypeptide, or an antibody to a human DPI or a human DPI-related polypeptide, is administered to a human subject for therapy (e.g. to ameliorate symptoms or to retard onset or progression) or prophylaxis.

5.14.1 Treatment And Prevention of BAD

Unipolar depression or BAD is treated or prevented by administration to a subject suspected of having or known to have BAD or to be at risk of developing BAD of a compound that modulates (i.e., increases or decreases) the level or activity (i.e., function) of one or more DPIs -- or the level of one or more DFs -- that are differentially present in the CSF of subjects having BAD compared with CSF of subjects free from BAD. In one embodiment, BAD is treated or prevented by administering to a subject suspected of having or known to have BAD or to be at risk of developing BAD a compound that upregulates (i.e., increases) the level or activity (i.e., function) of one or more DPIs -- or the level of one or more DFs -- that are decreased in the CSF of subjects having BAD. In another embodiment, a compound is administered that downregulates the level or activity (i.e., function) of one or more DPIs -- or the level of one or more DFs -- that are increased in the CSF of subjects having BAD. Examples of such a compound include but are not limited to: DPIs,

DPI fragments and DPI-related polypeptides; nucleic acids encoding a DPI, a DPI fragment and a DPI-related polypeptide (e.g., for use in gene therapy); and, for those DPIs or DPI-related polypeptides with enzymatic activity, compounds or molecules known to modulate that enzymatic activity. Other compounds that can be used, e.g., DPI agonists, can be identified using *in vitro* assays.

BAD is also treated or prevented by administration to a subject suspected of having or known to have BAD or to be at risk of developing BAD of a compound that downregulates the level or activity of one or more DPIs -- or the level of one or more DFs -- that are increased in the CSF of subjects having BAD. In another embodiment, a compound is administered that upregulates the level or activity of one or more DPIs -- or the level of one or more DFs -- that are decreased in the CSF of subjects having BAD. Examples of such a compound include, but are not limited to, DPI antisense oligonucleotides, ribozymes, antibodies directed against DPIs, and compounds that inhibit the enzymatic activity of a DPI. Other useful compounds e.g., DPI antagonists and small molecule DPI antagonists, can be identified using *in vitro* assays.

In a preferred embodiment, therapy or prophylaxis is tailored to the needs of an individual subject. Thus, in specific embodiments, compounds that promote the level or function of one or more DPIs, or the level of one or more DFs, are therapeutically or prophylactically administered to a subject suspected of having or known to have BAD, in whom the levels or functions of said one or more DPIs, or levels of said one or more DFs, are absent or are decreased relative to a control or normal reference range. In further embodiments, compounds that promote the level or function of one or more DPIs, or the level of one or more DFs, are therapeutically or prophylactically administered to a subject suspected of having or known to have BAD in whom the levels or functions of said one or more DPIs, or levels of said one or more DFs, are increased relative to a control or to a reference range. In further embodiments, compounds that decrease the level or function of one or more DPIs, or the level of one or more DFs, are therapeutically or prophylactically administered to a subject suspected of having or known to have BAD in whom the levels or functions of said one or more DPIs, or levels of said one or more DFs, are increased relative to a control or to a reference range. In further embodiments, compounds that decrease the level or function of one or more DPIs, or the level of one or more DFs, are therapeutically or prophylactically administered to a subject suspected of having or known to have BAD in whom the levels or functions of said one or more DPIs, or

levels of said one or more DFs, are decreased relative to a control or to a reference range. The change in DPI function or level, or DF level, due to the administration of such compounds can be readily detected, e.g., by obtaining a sample (e.g., a sample of CSF, blood or urine or a tissue sample such as biopsy tissue) and assaying *in vitro* the levels of said DFs or the levels or activities of said DPIs, or the levels of mRNAs encoding said DPIs. or any combination of the foregoing. Such assays can be performed before and after the administration of the compound as described herein.

The compounds of the invention include but are not limited to any compound, e.g., a small organic molecule, protein, peptide, antibody, nucleic acid, etc. that restores the BAD DPI or DF profile towards normal with the proviso that such compound is not lithium, divalproex, carbamazepine, lamotrigine; antidepressants: tricyclic antidepressants (eg. Desipramine, chlorimipramine, nortriptyline), selective serotonin reuptake inhibitors (SSRIs including fluoxetine (Prozac), sertraltrine (Zoloft), paroxitene (Paxil), fluvoxamine (Luvox), and citalopram (Celexa)), MAOIs, bupropion (Wellbutrin), venlafaxine (Effexor), and mirtazapine (Remeron); and atypical antipsychotic agents: Clozapine, Olanzapine, Risperidone..

5.14.2 Gene Therapy

In a specific embodiment, nucleic acids comprising a sequence encoding a DPI, a DPI fragment, DPI-related polypeptide or fragment of a DPI-related polypeptide, are administered to promote DPI function by way of gene therapy. Gene therapy refers to administration to a subject of an expressed or expressible nucleic acid. In this embodiment, the nucleic acid produces its encoded polypeptide that mediates a therapeutic effect by promoting DPI function.

Any of the methods for gene therapy available in the art can be used according to the present invention. Exemplary methods are described below.

For general reviews of the methods of gene therapy, see Goldspiel et al., 1993, Clinical Pharmacy 12:488-505; Wu and Wu, 1991, Biotherapy 3:87-95; Tolstoshev, 1993, Ann. Rev. Pharmacol. Toxicol. 32:573-596; Mulligan, 1993, Science 260:926-932; and Morgan and Anderson, 1993, Ann. Rev. Biochem. 62:191-217; May, 1993, TIBTECH 11(5):155-215. Methods commonly known in the art of recombinant DNA technology which can be used are described in Ausubel et al. (eds.), 1993, Current Protocols in Molecular Biology, John Wiley & Sons, NY; and Kriegler, 1990, Gene Transfer and Expression, A Laboratory Manual, Stockton Press, NY.

In a preferred aspect, the compound comprises a nucleic acid encoding a DPI or fragment or chimeric protein thereof, said nucleic acid being part of an expression vector that expresses a DPI or fragment or chimeric protein thereof in a suitable host. In particular, such a nucleic acid has a promoter operably linked to the DPI coding region, said promoter being inducible or constitutive (and, optionally, tissue-specific). In another particular embodiment, a nucleic acid molecule is used in which the DPI coding sequences and any other desired sequences are flanked by regions that promote homologous recombination at a desired site in the genome, thus providing for intrachromosomal expression of the DPI nucleic acid (Koller and Smithies, 1989, Proc. Natl. Acad. Sci. USA 86:8932-8935; Zijlstra et al., 1989, Nature 342:435-438).

Delivery of the nucleic acid into a subject may be direct, in which case the subject is directly exposed to the nucleic acid or nucleic acid-carrying vector; this approach is known as *in vivo* gene therapy. Alternatively, delivery of the nucleic acid into the subject may be indirect, in which case cells are first transformed with the nucleic acid *in vitro* and then transplanted into the subject; this approach is known as ex vivo gene therapy.

In a specific embodiment, the nucleic acid is directly administered *in vivo*, where it is expressed to produce the encoded product. This can be accomplished by any of numerous methods known in the art, e.g., by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, e.g., by infection using a defective or attenuated retroviral or other viral vector (see U.S. Patent No. 4,980,286); by direct injection of naked DNA; by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont); by coating with lipids, cell-surface receptors or transfecting agents; by encapsulation in liposomes, microparticles or microcapsules; by administering it in linkage to a peptide which is known to enter the nucleus; or by administering it in linkage to a ligand subject to receptor-mediated endocytosis (see, e.g., Wu and Wu, 1987, J. Biol. Chem. 262:4429-4432), which can be used to target cell types specifically expressing the receptors. In another embodiment, a nucleic acid-ligand complex can be formed in which the ligand comprises a fusogenic viral peptide to disrupt endosomes, allowing the nucleic acid to avoid lysosomal degradation. In yet another embodiment, the nucleic acid can be targeted *in vivo* for cell specific uptake and expression, by targeting a specific receptor (see, e.g., PCT Publications WO 92/06180 dated April 16, 1992 (Wu et al.); WO 92/22635 dated December 23, 1992 (Wilson et al.); WO92/20316 dated

November 26, 1992 (Findeis et al.); WO93/14188 dated July 22, 1993 (Clarke et al.), WO 93/20221 dated October 14, 1993 (Young)). Alternatively, the nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination (Koller and Smithies, 1989, Proc. Natl. Acad. Sci. USA 86:8932-8935; Zijlstra et al., 1989, Nature 342:435-438).

In a specific embodiment, a viral vector that contains a nucleic acid encoding a DPI is used. For example, a retroviral vector can be used (see Miller et al., 1993, Meth. Enzymol. 217:581-599). These retroviral vectors have been modified to delete retroviral sequences that are not necessary for packaging of the viral genome and integration into host cell DNA. The nucleic acid encoding the DPI to be used in gene therapy is cloned into the vector, which facilitates delivery of the gene into a subject. More detail about retroviral vectors can be found in Boesen et al., 1994, Biotherapy 6:291-302, which describes the use of a retroviral vector to deliver the mdr1 gene to hematopoietic stem cells in order to make the stem cells more resistant to chemotherapy. Other references illustrating the use of retroviral vectors in gene therapy are: Clowes et al., 1994, J. Clin. Invest. 93:644-651; Kiem et al., 1994, Blood 83:1467- 1473; Salmons and Gunzberg, 1993, Human Gene Therapy 4:129-141; and Grossman and Wilson, 1993, Curr. Opin. in Genetics and Devel. 3:110-114.

Adenoviruses are other viral vectors that can be used in gene therapy. Adenoviruses are especially attractive vehicles for delivering genes to respiratory epithelia. Adenoviruses naturally infect respiratory epithelia where they cause a mild disease. Other targets for adenovirus-based delivery systems are liver, the central nervous system, endothelial cells, and muscle. Adenoviruses have the advantage of being capable of infecting non-dividing cells. Kozarsky and Wilson, 1993, Current Opinion in Genetics and Development 3:499-503 present a review of adenovirus-based gene therapy. Bout et al., 1994, Human Gene Therapy 5:3-10 demonstrated the use of adenovirus vectors to transfer genes to the respiratory epithelia of rhesus monkeys. Other instances of the use of adenoviruses in gene therapy can be found in Rosenfeld et al., 1991, Science 252:431-434; Rosenfeld et al., 1992, Cell 68:143-155; Mastrangeli et al., 1993, J. Clin. Invest. 91:225-234; PCT Publication WO94/12649; and Wang, et al., 1995, Gene Therapy 2:775-783.

Adeno-associated virus (AAV) has also been proposed for use in gene therapy (Walsh et al., 1993, Proc. Soc. Exp. Biol. Med. 204:289-300; U.S. Patent No. 5,436,146).

Another approach to gene therapy involves transferring a gene to cells in tissue culture by such methods as electroporation, lipofection, calcium phosphate mediated transfection, or viral infection. Usually, the method of transfer includes the transfer of a selectable marker to the cells. The cells are then placed under selection to isolate those cells that have taken up and are expressing the transferred gene. Those cells are then delivered to a subject.

In this embodiment, the nucleic acid is introduced into a cell prior to administration *in vivo* of the resulting recombinant cell. Such introduction can be carried out by any method known in the art, including but not limited to transfection, electroporation, microinjection, infection with a viral or bacteriophage vector containing the nucleic acid sequences, cell fusion, chromosome-mediated gene transfer, microcell- mediated gene transfer, spheroplast fusion, etc. Numerous techniques are known in the art for the introduction of foreign genes into cells (see, e.g., Loeffler and Behr, 1993, Meth. Enzymol. 217:599-618; Cohen et al., 1993, Meth. Enzymol. 217:618-644; Cline, 1985, Pharmac. Ther. 29:69-92) and may be used in accordance with the present invention, provided that the necessary developmental and physiological functions of the recipient cells are not disrupted. The technique should provide for the stable transfer of the nucleic acid to the cell, so that the nucleic acid is expressible by the cell and preferably heritable and expressible by its cell progeny.

The resulting recombinant cells can be delivered to a subject by various methods known in the art. In a preferred embodiment, epithelial cells are injected, e.g., subcutaneously. In another embodiment, recombinant skin cells may be applied as a skin graft onto the subject. Recombinant blood cells (e.g., hematopoietic stem or progenitor cells) are preferably administered intravenously. The amount of cells envisioned for use depends on the desired effect, the condition of the subject, etc., and can be determined by one skilled in the art.

Cells into which a nucleic acid can be introduced for purposes of gene therapy encompass any desired, available cell type, and include but are not limited to neuronal cells, glial cells (e.g., oligodendrocytes or astrocytes), epithelial cells, endothelial cells, keratinocytes, fibroblasts, muscle cells, hepatocytes; blood cells such as T lymphocytes, B lymphocytes, monocytes, macrophages, neutrophils, eosinophils, megakaryocytes, granulocytes; various stem or progenitor cells, in particular

hematopoietic stem or progenitor cells, e.g., as obtained from bone marrow, umbilical cord blood, peripheral blood or fetal liver.

In a preferred embodiment, the cell used for gene therapy is autologous to the subject that is treated.

In an embodiment in which recombinant cells are used in gene therapy, a nucleic acid encoding a DPI is introduced into the cells such that it is expressible by the cells or their progeny, and the recombinant cells are then administered *in vivo* for therapeutic effect. In a specific embodiment, stem or progenitor cells are used. Any stem or progenitor cells which can be isolated and maintained *in vitro* can be used in accordance with this embodiment of the present invention (see e.g. PCT Publication WO 94/08598, dated April 28, 1994; Stemple and Anderson, 1992, Cell 71:973-985; Rheinwald, 1980, Meth. Cell Bio. 21A:229; and Pittelkow and Scott, 1986, Mayo Clinic Proc. 61:771).

In a specific embodiment, the nucleic acid to be introduced for purposes of gene therapy comprises an inducible promoter operably linked to the coding region, such that expression of the nucleic acid is controllable by controlling the presence or absence of the appropriate inducer of transcription.

Direct injection of a DNA coding for a DPI may also be performed according to, for example, the techniques described in United States Patent No. 5,589,466. These techniques involve the injection of "naked DNA", i.e., isolated DNA molecules in the absence of liposomes, cells, or any other material besides a suitable carrier. The injection of DNA encoding a protein and operably linked to a suitable promoter results in the production of the protein in cells near the site of injection and the elicitation of an immune response in the subject to the protein encoded by the injected DNA. In a preferred embodiment, naked DNA comprising (a) DNA encoding a DPI and (b) a promoter are injected into a subject to elicit an immune response to the DPI.

5.14.3 Inhibition of DPIs To Treat BAD

In one embodiment of the invention, BAD is treated or prevented by administration of a compound that antagonizes (inhibits) the level(s) and/or function(s) of one or more DPIs which are elevated in the CSF of subjects having BAD as compared with CSF of subjects free from Unipolar depression or BAD. Compounds useful for this purpose include but are not limited to anti-DPI antibodies (and fragments and derivatives containing the binding region thereof), DPI antisense or ribozyme nucleic acids, and nucleic acids encoding dysfunctional DPIs that are

used to "knockout" endogenous DPI function by homologous recombination (see, e.g., Capecchi, 1989, Science 244:1288-1292). Other compounds that inhibit DPI function can be identified by use of known *in vitro* assays, e.g., assays for the ability of a test compound to inhibit binding of a DPI to another protein or a binding partner, or to inhibit a known DPI function. Preferably such inhibition is assayed *in vitro* or in cell culture, but genetic assays may also be employed. The Preferred Technology can also be used to detect levels of the DPI before and after the administration of the compound. Preferably, suitable *in vitro* or *in vivo* assays are utilized to determine the effect of a specific compound and whether its administration is indicated for treatment of the affected tissue, as described in more detail below.

In a specific embodiment, a compound that inhibits a DPI function is administered therapeutically or prophylactically to a subject in whom an increased CSF level or functional activity of the DPI (e.g., greater than the normal level or desired level) is detected as compared with CSF of subjects free from Unipolar depression or BAD or a predetermined reference range. Methods standard in the art can be employed to measure the increase in a DPI level or function, as outlined above. Preferred DPI inhibitor compositions include small molecules, i.e., molecules of 1000 daltons or less. Such small molecules can be identified by the screening methods described herein.

5.14.4 Antisense Regulation of DPIs

In a specific embodiment, DPI expression is inhibited by use of DPI antisense nucleic acids. The present invention provides the therapeutic or prophylactic use of nucleic acids comprising at least six nucleotides that are antisense to a gene or cDNA encoding a DPI or a portion thereof. As used herein, a DPI "antisense" nucleic acid refers to a nucleic acid capable of hybridizing by virtue of some sequence complementarity to a portion of an RNA (preferably mRNA) encoding a DPI. The antisense nucleic acid may be complementary to a coding and/or noncoding region of an mRNA encoding a DPI. Such antisense nucleic acids have utility as compounds that inhibit DPI expression, and can be used in the treatment or prevention of BAD.

The antisense nucleic acids of the invention are double-stranded or single-stranded oligonucleotides, RNA or DNA or a modification or derivative thereof, and can be directly administered to a cell or produced intracellularly by transcription of exogenous, introduced sequences.

The invention further provides pharmaceutical compositions comprising an effective amount of the DPI antisense nucleic acids of the invention in a pharmaceutically acceptable carrier, as described infra.

In another embodiment, the invention provides methods for inhibiting the expression of a DPI nucleic acid sequence in a prokaryotic or eukaryotic cell comprising providing the cell with an effective amount of a composition comprising a DPI antisense nucleic acid of the invention.

DPI antisense nucleic acids and their uses are described in detail below.

5.14.4.1 DPI Antisense Nucleic Acids

The DPI antisense nucleic acids are of at least six nucleotides and are preferably oligonucleotides ranging from 6 to about 50 oligonucleotides. In specific aspects, the oligonucleotide is at least 10 nucleotides, at least 15 nucleotides, at least 100 nucleotides, or at least 200 nucleotides. The oligonucleotides can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof and can be single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone. The oligonucleotide may include other appended groups such as peptides; agents that facilitate transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. USA 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. WO 88/09810, published December 15, 1988) or blood-brain barrier (see, e.g., PCT Publication No. WO 89/10134, published April 25, 1988); hybridization-triggered cleavage agents (see, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents (see, e.g., Zon, 1988, Pharm. Res. 5:539-549).

In a preferred aspect of the invention, a DPI antisense oligonucleotide is provided, preferably of single-stranded DNA. The oligonucleotide may be modified at any position on its structure with substituents generally known in the art.

The DPI antisense oligonucleotide may comprise at least one of the following modified base moieties: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-

methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta- D-mannosylqueosine, 5′-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, 2,6-diaminopurine, and other base analogs.

In another embodiment, the oligonucleotide comprises at least one modified sugar moiety, e.g., one of the following sugar moieties: arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the oligonucleotide comprises at least one of the following modified phosphate backbones: a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, a formacetal, or an analog of formacetal.

In yet another embodiment, the oligonucleotide is an α-anomeric oligonucleotide. An α-anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gautier et al., 1987, Nucl. Acids Res. 15:6625-6641).

The oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport agent, or hybridization-triggered cleavage agent.

Oligonucleotides of the invention may be synthesized by standard methods known in the art, e.g., by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al. (1988, Nucl. Acids Res. 16:3209), and methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., 1988, Proc. Natl. Acad. Sci. USA 85:7448-7451).

In a specific embodiment, the DPI antisense nucleic acid of the invention is produced intracellularly by transcription from an exogenous sequence. For example, a vector can be introduced *in vivo* such that it is taken up by a cell, within which cell the vector or a portion thereof is transcribed, producing an antisense nucleic acid

(RNA) of the invention. Such a vector would contain a sequence encoding the DPI antisense nucleic acid. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology standard in the art. Vectors can be plasmid, viral, or others known in the art, used for replication and expression in mammalian cells. Expression of the sequence encoding the DPI antisense RNA can be by any promoter known in the art to act in mammalian, preferably human, cells. Such promoters can be inducible or constitutive. Examples of such promoters are outlined above.

The antisense nucleic acids of the invention comprise a sequence complementary to at least a portion of an RNA transcript of a gene encoding a DPI, preferably a human gene encoding a DPI. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," as referred to herein, means a sequence having sufficient complementarity to be able to hybridize under stringent conditions (e.g., highly stringent conditions comprising hybridization in 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65 C and washing in 0.1xSSC/0.1% SDS at 68 °C, or moderately stringent conditions comprising washing in 0.2xSSC/0.1% SDS at 42 °C) with the RNA, forming a stable duplex; in the case of double-stranded DPI antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA encoding a DPI it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

5.14.4.2 Therapeutic Use of DPI Antisense Nucleic Acids

The DPI antisense nucleic acids can be used to treat or prevent BAD when the target DPI is overexpressed in the CSF of subjects suspected of having or suffering from BAD. In a preferred embodiment, a single-stranded DNA antisense DPI oligonucleotide is used.

Cell types which express or overexpress RNA encoding a DPI can be identified by various methods known in the art. Such cell types include but are not limited to leukocytes (e.g., neutrophils, macrophages, monocytes) and resident cells (e.g., astrocytes, glial cells, neuronal cells, and ependymal cells). Such methods include, but are not limited to, hybridization with a DPI-specific nucleic acid (e.g., by Northern hybridization, dot blot hybridization, in situ hybridization), observing the ability of RNA from the cell type to be translated *in vitro* into a DPI, immunoassay, etc. In a preferred aspect, primary tissue from a subject can be assayed for DPI expression prior to treatment, e.g., by immunocytochemistry or in situ hybridization.

Pharmaceutical compositions of the invention, comprising an effective amount of a DPI antisense nucleic acid in a pharmaceutically aeceptable carrier, can be administered to a subject having BAD.

The amount of DPI antisense nucleic acid which will be effective in the treatment of BAD can be determined by standard clinical techniques.

In a specific embodiment, pharmaceutical compositions comprising one or more DPI antisense nucleic acids are administered via liposomes, microparticles, or microcapsules. In various embodiments of the invention, such compositions may be used to achieve sustained release of the DPI antisense nucleic acids.

5.14.5 Inhibitory Ribozyme and Triple Helix Approaches

In another embodiment, symptoms of BAD may be ameliorated by decreasing the level of a DPI or DPI activity by using gene sequences encoding the DPI in conjunction with well-known gene "knock-out," ribozyme or triple helix methods to decrease gene expression of a DPI. In this approach ribozyme or triple helix molecules are used to modulate the activity, expression or synthesis of the gene encoding the DPI, and thus to ameliorate the symptoms of BAD. Such molecules may be designed to reduce or inhibit expression of a mutant or non-mutant target gene. Techniques for the production and use of such molecules are well known to those of skill in the art.

Ribozyme molecules designed to catalytically cleave gene mRNA transcripts encoding a DPI can be used to prevent translation of target gene mRNA and, therefore, expression of the gene product. (See, e.g., PCT International Publication WO90/11364, published October 4, 1990; Sarver et al., 1990, Science 247:1222-1225).

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. (For a review, see Rossi, 1994, Current Biology 4, 469-471). The mechanism of ribozyme action involves sequence specific hybridization of the ribozyme molecule to complementary target RNA, followed by an endonucleolytic cleavage event. The composition of ribozyme molecules must include one or more sequences complementary to the target gene mRNA, and must include the well known catalytic sequence responsible for mRNA cleavage. For this sequence, see, e.g., U.S. Patent No. 5,093,246, which is incorporated herein by reference in its entirety.

While ribozymes that cleave mRNA at site specific recognition sequences can be used to destroy mRNAs encoding a DPI, the use of hammerhead ribozymes is preferred. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Myers, 1995, Molecular Biology and Biotechnology: A Comprehensive Desk Reference, VCH Publishers, New York, (see especially Figure 4, page 833) and in Haseloff and Gerlach, 1988, Nature, 334, 585-591, each of which is incorporated herein by reference in its entirety.

Preferably the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the mRNA encoding the DPI, i.e., to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts.

The ribozymes of the present invention also include RNA endoribonucleases (hereinafter "Cech-type ribozymes") such as the one that occurs naturally in Tetrahymena thermophila (known as the IVS, or L-19 IVS RNA) and that has been extensively described by Thomas Cech and collaborators (Zaug, et al., 1984, Science, 224, 574-578; Zaug and Cech, 1986, Science, 231, 470-475; Zaug, et al., 1986, Nature, 324, 429-433; published International patent application No. WO 88/04300 by University Patents Inc.; Been and Cech, 1986, Cell, 47, 207-216). The Cech-type ribozymes have an eight base pair active site which hybridizes to a target RNA sequence whereafter cleavage of the target RNA takes place. The invention encompasses those Cech-type ribozymes which target eight base-pair active site sequences that are present in the gene encoding the DPI.

As in the antisense approach, the ribozymes can be composed of modified oligonucleotides (e.g., for improved stability, targeting, etc.) and should be delivered

to cells that express the DPI *in vivo*. A preferred method of delivery involves using a DNA construct "encoding" the ribozyme under the control of a strong constitutive pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to destroy endogenous mRNA encoding the DPI and inhibit translation. Because ribozymes, unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficacy.

Endogenous DPI expression can also be reduced by inactivating or "knocking out" the gene encoding the DPI, or the promoter of such a gene, using targeted homologous recombination (e.g., see Smithies, et al., 1985, Nature 317:230-234; Thomas and Capecchi, 1987, Cell 51:503-512; Thompson et al., 1989, Cell 5:313-321; and Zijlstra et al., 1989, Nature 342:435-438, each of which is incorporated by reference herein in its entirety). For example, a mutant gene encoding a non-functional DPI (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous gene (either the coding regions or regulatory regions of the gene encoding the DPI) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express the target gene *in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the target gene. Such approaches are particularly suited in the agricultural field where modifications to ES (embryonic stem) cells can be used to generate animal offspring with an inactive target gene (e.g., see Thomas and Capecchi, 1987 and Thompson, 1989, supra). However this approach can be adapted for use in humans provided the recombinant DNA constructs are directly administered or targeted to the required site *in vivo* using appropriate viral vectors.

Alternatively, the endogenous expression of a gene encoding a DPI can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of the gene (i.e., the gene promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene encoding the DPI in target cells in the body. (See generally, Helene, 1991, Anticancer Drug Des., 6(6), 569-584; Helene, et al., 1992, Ann. N.Y. Acad. Sci., 660, 27-36; and Maher, 1992, Bioassays 14(12), 807-815).

Nucleic acid molecules to be used in triplex helix formation for the inhibition of transcription should be single stranded and composed of deoxynucleotides. The base composition of these oligonucleotides must be designed to promote triple helix formation via Hoogsteen base pairing rules, which generally require sizeable stretches

of either purines or pyrimidines to be present on one strand of a duplex. Nucleotide sequences may be pyrimidine-based, which will result in TAT and CGC+ triplets across the three associated strands of the resulting triple helix. The pyrimidine-rich molecules provide base complementarity to a purine-rich region of a single strand of the duplex in a parallel orientation to that strand. In addition, nucleic acid molecules may be chosen that are purine-rich, for example, contain a stretch of G residues. These molecules will form a triple helix with a DNA duplex that is rich in GC pairs, in which the majority of the purine residues are located on a single strand of the targeted duplex, resulting in GGC triplets across the three strands in the triplex.

Alternatively, the potential sequences that can be targeted for triple helix formation may be increased by creating a so called "switchback" nucleic acid molecule. Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with first one strand of a duplex and then the other, eliminating the necessity for a sizeable stretch of either purines or pyrimidines to be present on one strand of a duplex.

In instances wherein the antisense, ribozyme, or triple helix molecules described herein are utilized to inhibit mutant gene expression, it is possible that the technique may so efficiently reduce or inhibit the transcription (triple helix) or translation (antisense, ribozyme) of mRNA produced by normal gene alleles of a DPI that the situation may arise wherein the concentration of DPI present may be lower than is necessary for a normal phenotype. In such cases, to ensure that substantially normal levels of activity of a gene encoding a DPI are maintained, gene therapy may be used to introduce into cells nucleic acid molecules that encode and express the DPI that exhibit normal gene activity and that do not contain sequences susceptible to whatever antisense, ribozyme, or triple helix treatments are being utilized. Alternatively, in instances whereby the gene encodes an extracellular protein, normal DPI can be co- administered in order to maintain the requisite level of DPI activity.

Antisense RNA and DNA, ribozyme, and triple helix molecules of the invention may be prepared by any method known in the art for the synthesis of DNA and RNA molecules, as discussed above. These include techniques for chemically synthesizing oligodeoxyribonucleotides and oligoribonucleotides well known in the art such as for example solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may

be incorporated into a wide variety of vectors that incorporate suitable RNA polymerase promoters such as the T7 or SP6 polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

5.15 Assays For Therapeutic Or Prophylactic Compounds

The present invention also provides assays for use in drug discovery in order to identify or verify the efficacy of compounds for treatment or prevention of BAD. Test compounds can be assayed for their ability to restore DF or DPI levels in a subject having BAD towards levels found in subjects free from BAD or to produce similar changes in experimental animal models of BAD. Compounds able to restore DF or DPI levels in a subject having BAD towards levels found in subjects free from BAD or to produce similar changes in experimental animal models of BAD can be used as lead compounds for further drug discovery, or used therapeutically. DF and DPI expression can be assayed by the Preferred Technology, immunoassays, gel electrophoresis followed by visualization, detection of DPI activity, or any other method taught herein or known to those skilled in the art. Such assays can be used to screen candidate drugs, in clinical monitoring or in drug development, where abundance of a DF or DPI can serve as a surrogate marker for clinical disease.

In various specific embodiments, *in vitro* assays can be carried out with cells representative of cell types involved in a subject's disorder, to determine if a compound has a desired effect upon such cell types.

Compounds for use in therapy can be tested in suitable animal model systems prior to testing in humans, including but not limited to rats, mice, chicken, cows, monkeys, rabbits, etc. For *in vivo* testing, prior to administration to humans, any animal model system known in the art may be used. Examples of animal models of BAD include, but are not limited to, animals that express human familial BAD genes and the Porsolt forced swim test model of depression is frequently used in both these contexts (Kirby and Lucki, 1997; Rossetti et al., 1993). The two major clinical states observed in bipolar disorder (depression and mania) have also been successfully modeled (Cappeliez and Moore Prog Neuropsychopharmacol Biol Psychiatry 1990 14, 347-58). Psychostimulant treatment can produce a range of behaviors similar to that of mania including hyperactivity, heightened sensory awareness, and alertness, and for this reason has become a very useful model for mania which exhibits (to some

extent) face, construct and predictive validity. Another model that has been utilized for the development of bipolar illness is behavioral sensitization. In this model, the repeated administration of many psychostimulant drugs leads to a gradual increase or sensitization of the drug-induced behavioral; this model also has considerable construct and face validity for mania (Koob et al. Pharmacol Biochem Behav 1997 57, 513-21)), which can be utilised to test compounds that modulate DF or DPI levels. It is also apparent to the skilled artisan that, based upon the present disclosure, transgenic animals can be produced with "knock-out" mutations of the gene or genes encoding one or more DPIs. A "knock-out" mutation of a gene is a mutation that causes the mutated gene to not be expressed, or expressed in an aberrant form or at a low level, such that the activity associated with the gene product is nearly or entirely absent. Preferably, the transgenic animal is a mammal, more preferably, the transgenic animal is a mouse.

In one embodiment, test compounds that modulate the expression of a DPI are identified in non-human animals (e.g., mice, rats, monkeys, rabbits, and guinea pigs), preferably non-human animal models for BAD, expressing the DPI. In accordance with this embodiment, a test compound or a control compound is administered to the animals, and the effect of the test compound on expression of one or more DPIs is determined. A test compound that alters the expression of a DPI (or a plurality of DPIs) can be identified by comparing the level of the selected DPI or DPIs (or mRNA(s) encoding the same) in an animal or group of animals treated with a test compound with the level of the DPI(s) or mRNA(s) in an animal or group of animals treated with a control compound. Techniques known to those of skill in the art can be used to determine the mRNA and protein levels, for example, in situ hybridization. The animals may or may not be sacrificed to assay the effects of a test compound.

In another embodiment, test compounds that modulate the activity of a DPI or a biologically active portion thereof are identified in non-human animals (e.g., mice, rats, monkeys, rabbits, and guinea pigs), preferably non-human animal models for BAD, expressing the DPI. In accordance with this embodiment, a test compound or a control compound is administered to the animals, and the effect of a test compound on the activity of a DPI is determined. A test compound that alters the activity of a DPI (or a plurality of DPIs) can be identified by assaying animals treated with a control compound and animals treated with the test compound. The activity of the DPI can be assessed by detecting induction of a cellular second messenger of the DPI (e.g.,

intracellular Ca2+, diacylglycerol, IP3, etc.), detecting catalytic or enzymatic activity of the DPI or binding partner thereof, detecting the induction of a reporter gene (e.g., a regulatory element that is responsive to a DPI of the invention operably linked to a nucleic acid encoding a detectable marker, such as luciferase or green fluorescent protein), or detecting a cellular response (e.g., cellular differentiation or cell proliferation). Techniques known to those of skill in the art can be utilized to detect changes in the activity of a DPI (see, e.g., U.S. Patent No. 5,401,639, which is incorporated herein by reference).

In yet another embodiment, test compounds that modulate the level or expression of a DPI (or plurality of DPIs) are identified in human subjects having BAD, preferably those having mild to severe BAD and most preferably those having mild BAD. In accordance with this embodiment, a test compound or a control compound is administered to the human subject, and the effect of a test compound on DPI expression is determined by analyzing the expression of the DPI or the mRNA encoding the same in a biological sample (e.g., CSF, serum, plasma, or urine). A test compound that alters the expression of a DPI can be identified by comparing the level of the DPI or mRNA encoding the same in a subject or group of subjects treated with a control compound to that in a subject or group of subjects treated with a test compound. Alternatively, alterations in the expression of a DPI can be identified by comparing the level of the DPI or mRNA encoding the same in a subject or group of subjects before and after the administration of a test compound. Techniques known to those of skill in the art can be used to obtain the biological sample and analyze the mRNA or protein expression. For example, the Preferred Technology described herein can be used to assess changes in the level of a DPI.

In another embodiment, test compounds that modulate the activity of a DPI (or plurality of DPIs) are identified in human subjects having BAD, preferably those having mild to severe BAD and most preferably those with mild BAD. In this embodiment, a test compound or a control compound is administered to the human subject, and the effect of a test compound on the activity of a DPI is determined. A test compound that alters the activity of a DPI can be identified by comparing biological samples from subjects treated with a control compound to samples from subjects treated with the test compound. Alternatively, alterations in the activity of a DPI can be identified by comparing the activity of a DPI in a subject or group of subjects before and after the administration of a test compound. The activity of the

DPI can be assessed by detecting in a biological sample (e.g., CSF, serum, plasma, or urine) induction of a cellular signal transduction pathway of the DPI (e.g., intracellular Ca2+, diacylglycerol, IP3, etc.), catalytic or enzymatic activity of the DPI or a binding partner thereof, or a cellular response, for example, cellular differentiation, or cell proliferation. Techniques known to those of skill in the art can be used to detect changes in the induction of a second messenger of a DPI or changes in a cellular response. For example, RT-PCR can be used to detect changes in the induction of a cellular second messenger.

In a preferred embodiment, a test compound that changes the level or expression of a DPI towards levels detected in control subjects (e.g., humans free from BAD) is selected for further testing or therapeutic use. In another preferred embodiment, a test compound that changes the activity of a DPI towards the activity found in control subjects (e.g., humans free from BAD) is selected for further testing or therapeutic use.

In another embodiment, test compounds that reduce the severity of one or more symptoms associated with BAD are identified in human subjects having BAD, preferably subjects having mild to severe BAD and most preferably subjects with mild BAD. In accordance with this embodiment, a test compound or a control compound is administered to the subjects, and the effect of a test compound on one or more symptoms of BAD is determined. A test compound that reduces one or more symptoms can be identified by comparing the subjects treated with a control compound to the subjects treated with the test compound. Techniques known to physicians familiar with BAD can be used to determine whether a test compound reduces one or more symptoms associated with BAD. For example, a test compound that enhances memory or reduces confusion in a subject having BAD will be beneficial for treating subjects having BAD.

In a preferred embodiment, a test compound that reduces the severity of one or more symptoms associated with BAD in a human having BAD is selected for further testing or therapeutic use.

5.16 Therapeutic and Prophylactic Compositions and Their Use

The invention provides methods of treatment (and prophylaxis) comprising administering to a subject an effective amount of a compound of the invention. In a preferred aspect, the compound is substantially purified (e.g., substantially free from

substances that limit its effect or produce undesired side-effects). The subject is preferably an animal, including but not limited to animals such as cows, pigs, horses, chickens, cats, dogs, etc., and is preferably a mammal, and most preferably human. In a specific embodiment, a non-human mammal is the subject.

Formulations and methods of administration that can be employed when the compound comprises a nucleic acid are described above; additional appropriate formulations and routes of administration are described below.

Various delivery systems are known and can be used to administer a compound of the invention, e.g., encapsulation in liposomes, microparticles, microcapsules, recombinant cells capable of expressing the compound, receptor-mediated endocytosis (see, e.g., Wu and Wu, 1987, J. Biol. Chem. 262:4429-4432), construction of a nucleic acid as part of a retroviral or other vector, etc. Methods of introduction can be enteral or parenteral and include but are not limited to intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The compounds may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together with other biologically active agents. Administration can be systemic or local. In addition, it may be desirable to introduce the pharmaceutical compositions of the invention into the central nervous system by any suitable route, including intraventricular and intrathecal injection; intraventricular injection may be facilitated by an intraventricular catheter, for example, attached to a reservoir, such as an Ommaya reservoir. Pulmonary administration can also be employed, e.g., by use of an inhaler or nebulizer, and formulation with an aerosolizing agent.

In a specific embodiment, it may be desirable to administer the pharmaceutical compositions of the invention locally to the area in need of treatment; this may be achieved, for example, and not by way of limitation, by local infusion during surgery, topical application, e.g., by injection, by means of a catheter, or by means of an implant, said implant being of a porous, non-porous, or gelatinous material, including membranes, such as sialastic membranes, or fibers. In one embodiment, administration can be by direct injection into CSF or at the site (or former site) of neurodegeneration or to CNS tissue.

In another embodiment, the compound can be delivered in a vesicle, in particular a liposome (see Langer, 1990, Science 249:1527-1533; Treat et al., in

Liposomes in the Therapy of Infectious Disease and Cancer, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 353-365 (1989); Lopez-Berestein, ibid., pp. 317-327; see generally ibid.)

In yet another embodiment, the compound can be delivered in a controlled release system. In one embodiment, a pump may be used (see Langer, supra; Sefton, 1987, CRC Crit. Ref. Biomed. Eng. 14:201; Buchwald et al., 1980, Surgery 88:507; Saudek et al., 1989, N. Engl. J. Med. 321:574). In another embodiment, polymeric materials can be used (see Medical Applications of Controlled Release, Langer and Wise (eds.), CRC Pres., Boca Raton, Florida (1974); Controlled Drug Bioavailability, Drug Product Design and Performance, Smolen and Ball (eds.), Wiley, New York (1984); Ranger and Peppas, J., 1983, Macromol. Sci. Rev. Macromol. Chem. 23:61; see also Levy et al., 1985, Science 228:190; During et al., 1989, Ann. Neurol. 25:351; Howard et al., 1989, J. Neurosurg. 71:105). In yet another embodiment, a controlled release system can be placed in proximity of the therapeutic target, i.e., the brain, thus requiring only a fraction of the systemic dose (see, e.g., Goodson, in Medical Applications of Controlled Release, supra, vol. 2, pp. 115-138 (1984)).

Other controlled release systems are discussed in the review by Langer (1990, Science 249:1527-1533).

In a specific embodiment where the compound of the invention is a nucleic acid encoding a protein, the nucleic acid can be administered *in vivo* to promote expression of its encoded protein, by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, e.g., by use of a retroviral vector (see U.S. Patent No. 4,980,286), or by direct injection, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors or transfecting agents, or by administering it in linkage to a homeobox-like peptide which is known to enter the nucleus (see e.g., Joliot et al., 1991, Proc. Natl. Acad. Sci. USA 88:1864-1868), etc. Alternatively, a nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination.

The present invention also provides pharmaceutical compositions. Such compositions comprise a therapeutically effective amount of a compound, and a pharmaceutically acceptable carrier. In a specific embodiment, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized

pharmacopeia for use in animals, and more particularly in humans. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsion, tablets, pills, capsules, powders, sustained-release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin. Such compositions will contain a therapeutically effective amount of the compound, preferably in purified form, together with a suitable amount of carrier so as to provide the form for proper administration to the subject. The formulation should suit the mode of administration.

In a preferred embodiment, the composition is formulated in accordance with routine procedures as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic such as lidocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition

is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

The compounds of the invention can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with free amino groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and those formed with free carboxyl groups such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

The amount of the compound of the invention which will be effective in the treatment of BAD can be determined by standard clinical techniques. In addition, *in vitro* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each subject's circumstances. However, suitable dosage ranges for intravenous administration are generally about 20- 500 micrograms of active compound per kilogram body weight. Suitable dosage ranges for intranasal administration are generally about 0.01 pg/kg body weight to 1 mg/kg body weight. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

Suppositories generally contain active ingredient in the range of 0.5% to 10% by weight; oral formulations preferably contain 10% to 95% active ingredient.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects (a) approval by the agency of manufacture, use or sale for human administration, (b) directions for use, or both.

6. EXAMPLE: IDENTIFICATION OF PROTEINS DIFFERENTIALLY EXPRESSED IN THE CSF IN BAD

Using the following procedure, proteins in CSF samples from five subjects having BAD and five control subjects were separated by isoelectric focusing followed by SDS- PAGE and analyzed. From some subjects, serial samples were taken over

time. Parts 6.1.1 to 6.1.9 (inclusive) of the procedure set forth below are hereby designated as the "Reference Protocol".

6.1. MATERIALS AND METHODS

6.1.1 Sample Preparation

A protein assay (Pierce BCA Cat # 23225) was performed on each CSF sample as received. Prior to protein separation, each sample was processed for selective depletion of certain proteins, in order to enhance and simplify protein separation and facilitate analysis by removing proteins that may interfere with or limit analysis of proteins of interest. See International Patent Application No. PCT/GB99/01742, filed June 1, 1999, which is incorporated by reference in its entirety, with particular reference to pages 3 and 6.

Removal of albumin, haptoglobin, transferrin and immunoglobin G (IgG) from CSF ("CSF depletion") was achieved by an affinity chromatography purification step in which the sample was passed through a series of 'Hi-Trap' columns containing immobilized antibodies for selective removal of albumin, haptoglobin and transferrin, and protein G for selective removal of immunoglobin G. Two affinity columns in a tandem assembly were prepared by coupling antibodies to protein G-sepharose contained in Hi-Trap columns (Protein G-Sepharose Hi-Trap columns (1 ml) Pharmacia Cat. No. 17-0404-01). This was done by circulating the following solutions sequentially through the columns: (1) Dulbecco's Phosphate Buffered Saline (Gibco BRL Cat. No. 14190-094); (2) concentrated antibody solution; (3) 200 mM sodium carbonate buffer, pH 8.35; (4) cross-linking solution (200 mM sodium carbonate buffer, pH 8.35, 20 mM dimethylpimelimidate); and (5) 500 mM ethanolamine, 500 mM NaCl. A third (un-derivatised) protein G Hi-Trap column was then attached to the lower end of the tandem column assembly.

The chromatographic procedure was automated using an Akta Fast Protein Liquid Chromatography (FPLC) System such that a series of up to seven runs could be performed sequentially. The samples were passed through the series of 3 Hi-Trap columns in which the affinity chromatography media selectively bind the above proteins thereby removing them from the sample. Fractions (typically 3 ml per tube) were collected of unbound material ("Flowthrough fractions") that eluted through the column during column loading and washing stages and of bound proteins

("Bound/Eluted fractions") that were eluted by step elution with Immunopure Gentle Ag/Ab Elution Buffer (Pierce Cat. No. 21013). The eluate containing unbound material was collected in fractions which were pooled, desalted/concentrated by centrifugal ultrafiltration and stored to await further analysis by 2D PAGE.

A volume of depleted CSF containing approximately 100-150 µg of total protein was aliquoted and an equal volume of 10% (w/v) SDS (Fluka 71729), 2.3% (w/v) dithiothreitol (BDH 443852A) was added. The sample was heated at 95 °C for 5 mins, and then allowed to cool to 20 °C . 125µl of the following buffer was then added to the sample:

8M urea (BDH 452043w)

4% CHAPS (Sigma C3023)

65mM dithiotheitol (DTT)

2% (v/v) Resolytes 3.5-10 (BDH 44338 2x) This mixture was vortexed, and centrifuged at 13000 rpm for 5 mins at 15 °C, and the supernatant was separated by isoelectric focusing as described below.

6.1.2 Isoelectric Focusing

Isoelectric focusing (IEF), was performed using the Immobiline® DryStrip Kit (Pharmacia BioTech), following the procedure described in the manufacturer's instructions, see Instructions for Immobiline® DryStrip Kit, Pharmacia, # 18-1038-63, Edition AB (incorporated herein by reference in its entirety). Immobilized pH Gradient (IPG) strips (18cm, pH 3-10 non-linear strips; Pharmacia Cat. # 17-1235-01) were rehydrated overnight at 20 °C in a solution of 8M urea, 2% (w/v) CHAPS, 10mM DTT, 2% (v/v) Resolytes 3.5-10, as described in the Immobiline DryStrip Users Manual. For IEF, 50 µl of supernatant (prepared as above) was loaded onto a strip, with the cup- loading units being placed at the basic end of the strip. The loaded gels were then covered with mineral oil (Pharmacia 17-3335-01) and a voltage was immediately applied to the strips according to the following profile, using a Pharmacia EPS3500XL power supply (Cat 19-3500-01):

Initial voltage = 300V for 2 hrs

Linear Ramp from 300V to 3500V over 3hrs

Hold at 3500V for 19hrs For all stages of the process, the current limit was set to 10mA for 12 gels, and the wattage limit to 5W. The temperature was held at 20 °C throughout the run.

6.1.3 Gel Equilibration and SDS-PAGE

After the final 19hr step, the strips were immediately removed and immersed for 10 mins at 20 °C in a first solution of the following composition: 6M urea; 2% (w/v) DTT; 2% (w/v) SDS; 30% (v/v) glycerol (Fluka 49767); 0.05M Tris/HCl, pH 6.8 (Sigma Cat T-1503). The strips were removed from the first solution and immersed for 10 mins at 20 °C in a second solution of the following composition: 6M urea; 2% (w/v) iodoacetamide (Sigma I-6125); 2% (w/v) SDS; 30% (v/v) glycerol; 0.05M Tris/HCl, pH 6.8. After removal from the second solution, the strips were loaded onto supported gels for SDS-PAGE according to Hochstrasser et al., 1988, Analytical Biochemistry 173: 412-423 (incorporated herein by reference in its entirety), with modifications as specified below.

6.1.4 Preparation of supported gels

The gels were cast between two glass plates of the following dimensions: 23cm wide x 24cm long (back plate); 23cm wide x 24cm long with a 2cm deep notch in the central 19cm (front plate). To promote covalent attachment of SDS-PAGE gels, the back plate was treated with a 0.4% solution of γ-methacryl-oxypropyltrimethoxysilane in ethanol (BindSilane™; Pharmacia Cat. # 17-1330-01). The front plate was treated with (RepelSilane™ Pharmacia Cat. # 17-1332-01) to reduce adhesion of the gel. Excess reagent was removed by washing with water, and the plates were allowed to dry. At this stage, both as identification for the gel, and as a marker to identify the coated face of the plate, an adhesive bar-code was attached to the back plate in a position such that it would not come into contact with the gel matrix.

The dried plates were assembled into a casting box with a capacity of 13 gel sandwiches. The front and back plates of each sandwich were spaced by means of 1mm thick spacers, 2.5 cm wide. The sandwiches were interleaved with acetate sheets to facilitate separation of the sandwiches after gel polymerization. Casting was then carried out according to Hochstrasser et al., op. cit.

A 9-16% linear polyacrylamide gradient was cast, extending up to a point 2cm below the level of the notch in the front plate, using the Angelique gradient casting system (Large Scale Biology). Stock solutions were as follows. Acrylamide (40% in water) was from Serva (Cat. # 10677). The cross-linking agent was PDA (BioRad 161- 0202), at a concentration of 2.6% (w/w) of the total starting monomer content. The gel buffer was 0.375M Tris/HCl, pH 8.8. The polymerization catalyst was 0.05% (v/v) TEMED (BioRad 161-0801), and the initiator was 0.1% (w/v) APS (BioRad 161-0700). No SDS was included in the gel and no stacking gel was used. The cast gels were allowed to polymerize at 20 °C overnight, and then stored individually at 4 °C in sealed polyethylene bags with 6ml of gel buffer, and were used within 4 weeks.

6.1.5 SDS-PAGE

A solution of 0.5% (w/v) agarose (Fluka Cat 05075) was prepared in running buffer (0.025M Tris, 0.198M glycine (Fluka 50050), 1% (w/v) SDS, supplemented by a trace of bromophenol blue). The agarose suspension was heated to 70 °C with stirring, until the agarose had dissolved. The top of the supported 2nd D gel was filled with the agarose solution, and the equilibrated strip was placed into the agarose, and tapped gently with a palette knife until the gel was intimately in contact with the 2nd D gel. The gels were placed in the 2nd D running tank, as described by Amess et al., 1995, Electrophoresis 16: 1255-1267 (incorporated herein by reference in its entirety). The tank was filled with running buffer (as above) until the level of the buffer was just higher than the top of the region of the 2nd D gels which contained polyacrylamide, so as to achieve efficient cooling of the active gel area. Running buffer was added to the top buffer compartments formed by the gels, and then voltage was applied immediately to the gels using a Consort E-833 power supply. For 1 hour, the gels were run at 20mA/gel. The wattage limit was set to 150W for a tank containing 6 gels, and the voltage limit was set to 600V. After 1 hour, the gels were then run at 40mA/gel, with the same voltage and wattage limits as before, until the bromophenol blue line was 0.5cm from the bottom of the gel. The temperature of the buffer was held at 16 °C throughout the run. Gels were not run in duplicate.

6.1.6 Staining

Upon completion of the electrophoresis run, the gels were immediately removed from the tank for fixation. The top plate of the gel cassette was carefully removed, leaving the gel bonded to the bottom plate. The bottom plate with its attached gel was then placed into a staining apparatus, which can accommodate 12 gels. The gels were completely immersed in fixative solution of 40% (v/v) ethanol (BDH 28719), 10% (v/v) acetic acid (BDH 100016X), 50% (v/v) water (MilliQ-Millipore), which was continuously circulated over the gels. After an overnight incubation, the fixative was drained from the tank, and the gels were primed by immersion in 7.5% (v/v) acetic acid, 0.05% (w/v) SDS, 92.5% (v/v) water for 30 mins. The priming solution was then drained, and the gels were stained by complete immersion for 4 hours in a staining solution of Pyridinium, 4-[2-[4-(dipentylamino)-2-trifluoromethylphenyl] ethenyl]-1- (sulfobutyl)-, inner salt, prepared by diluting a stock solution of this dye (2mg/ml in DMSO) in 7.5% (v/v) aqueous acetic acid to give a final concentration of 1.2 mg/l; the staining solution was vacuum filtered through a 0.4μm filter (Duropore) before use.

6.1.7 Imaging of the gel

A computer-readable output was produced by imaging the fluorescently stained gels with the Apollo 2 scanner (Oxford Glycosciences, Oxford, UK) described in section 5.1, supra. This scanner has a gel carrier with four integral fluorescent markers (Designated M1, M2, M3) that are used to correct the image geometry and are a quality control feature to confirm that the scanning has been performed correctly.

For scanning, the gels were removed from the stain, rinsed with water and allowed to air dry briefly, and imaged on the Apollo 2. After imaging, the gels were sealed in polyethylene bags containing a small volume of staining solution, and then stored at 4 °C.

6.1.8 Digital Analysis of the Data

The data were processed as described in U.S. Application Patent No. 6,064,757 at Sections 5.4 and 5.5 (incorporated herein by reference), as set forth more particularly below.

The output from the scanner was first processed using the MELANIE® II 2D PAGE analysis program (Release 2.2, 1997, BioRad Laboratories, Hercules, California, Cat. # 170-7566) to autodetect the registration points, M1, M2, M3 and M4; to autocrop the images (i.e., to eliminate signals originating from areas of the scanned image lying outside the boundaries of the gel, e.g. the reference frame); to filter out artifacts due to dust; to detect and quantify features; and to create image files in GIF format. Features were detected using the following parameters:

Smooths =2

Laplacian threshold 50

Partials threshold 1

Saturation = 100

Peakedness = 0

Minimum Perimeter = 10

6.1.9 Assignment of pI and MW Values

Landmark identification was used to determine the pI and MW of features detected in the images. Twelve landmark features, designated CSF1 to CSF12, were identified in a standard CSF image obtained from a pooled sample. These landmark features are identified in Figure 1 and were assigned the pI and/or MW values identified in Table XIV.

Table XIV. Landmark Features Used In This Study

Name	pI	MW (Da)	Name	pI	MW (Da)
CSF1	5.96	185230	CSF7	4.78	41340
CSF2	5.39	141700	CSF8	9.20	40000
CSF3	6.29	100730	CSF9	5.50	31900
CSF4	5.06	71270	CSF10	6.94	27440
CSF5	7.68	68370	CSF11	5.90	23990
CSF6	5.67	48090	CSF12	6.43	10960

As many of these landmarks as possible were identified in each gel image of the dataset. Each feature in the study gels was then assigned a pI value by linear

interpolation or extrapolation (using the MELANIE®-II software) to the two nearest landmarks, and was assigned a MW value by linear interpolation or extrapolation (using the MELANIE®-II software) to the two nearest landmarks.

6.1.10 Matching With Primary Master Image

Images were edited to remove gross artifacts such as dust, to reject images which had gross abnormalities such as smearing of protein features, or were of too low a loading or overall image intensity to allow identification of more than the most intense features, or were of too poor a resolution to allow accurate detection of features. Images were then compared by pairing with one common image from the whole sample set. This common image, the "primary master image", was selected on the basis of protein load (maximum load consistent with maximum feature detection), a well resolved myoglobin region, (myoglobin was used as an internal standard), and general image quality. Additionally, the primary master image was chosen to be an image which appeared to be generally representative of all those to be included in the analysis. (This process by which a primary master gel was judged to be representative of the study gels was rechecked by the method described below and in the event that the primary master gel was seen to be unrepresentative, it was rejected and the process repeated until a representative primary master gel was found.)

Each of the remaining study gel images was individually matched to the primary master image such that common protein features were paired between the primary master image and each individual study gel image as described below.

6.1.11 Cross-matching Between Samples

To facilitate statistical analysis of large numbers of samples for purposes of identifying features that are differentially expressed, the geometry of each study gel was adjusted for maximum alignment between its pattern of protein features, and that of the primary master, as follows. Each of the study gel images was individually transformed into the geometry of the primary master image using a multi-resolution warping procedure. This procedure corrects the image geometry for the distortions brought about by small changes in the physical parameters of the electrophoresis separation process from one sample to another. The observed changes are such that the distortions found are not simple geometric distortions, but rather a smooth flow, with variations at both local and global scale.

The fundamental principle in multi-resolution modeling is that smooth signals may be modeled as an evolution through 'scale space', in which details at successively finer scales are added to a low resolution approximation to obtain the high resolution signal. This type of model is applied to the flow field of vectors (defined at each pixel position on the reference image) and allows flows of arbitrary smoothness to be modeled with relatively few degrees of freedom. Each image is first reduced to a stack, or pyramid, of images derived from the initial image, but smoothed and reduced in resolution by a factor of 2 in each direction at every level (Gaussian pyramid) and a corresponding difference image is also computed at each level, representing the difference between the smoothed image and its progenitor (Laplacian pyramid). Thus the Laplacian images represent the details in the image at different scales.

To estimate the distortion between any 2 given images, a calculation was performed at level 7 in the pyramid (i.e. after 7 successive reductions in resolution). The Laplacian images were segmented into a grid of 16x16 pixels, with 50% overlap between adjacent grid positions in both directions, and the cross correlation between corresponding grid squares on the reference and the test images was computed. The distortion displacement was then given by the location of the maximum in the correlation matrix. After all displacements had been calculated at a particular level, they were interpolated to the next level in the pyramid, applied to the test image, and then further corrections to the displacements were calculated at the next scale.

The warping process brought about good alignment between the common features in the primary master image, and the images for the other samples. The MELANIE® II 2D PAGE analysis program was used to calculate and record approximately 500-700 matched feature pairs between the primary master and each of the other images. The accuracy of this program was significantly enhanced by the alignment of the images in the manner described above. To improve accuracy still further, all pairings were finally examined by eye in the MelView interactive editing program and residual recognizably incorrect pairings were removed. Where the number of such recognizably incorrect pairings exceeded the overall reproducibility of the Preferred Technology (as measured by repeat analysis of the same biological sample) the gel selected to be the primary master gel was judged to be insufficiently representative of the study gels to serve as a primary master gel. In that case, the gel chosen as the primary master gel was rejected, and different gel was selected as the primary master gel, and the process was repeated.

All the images were then added together to create a composite master image, and the positions and shapes of all the gel features of all the component images were super- imposed onto this composite master as described below.

Once all the initial pairs had been computed, corrected and saved, a second pass was performed whereby the original (unwarped) images were transformed a second time to the geometry of the primary master, this time using a flow field computed by smooth interpolation of the multiple tie-points defined by the centroids of the paired gel features. A composite master image was thus generated by initialising the primary master image with its feature descriptors. As each image was transformed into the primary master geometry, it was digitally summed pixel by pixel into the composite master image, and the features that had not been paired by the procedure outlined above were likewise added to the composite master image description, with their centroids adjusted to the master geometry using the flow field correction.

The final stage of processing was applied to the composite master image and its feature descriptors, which now represent all the features from all the images in the study transformed to a common geometry. The features were grouped together into linked sets or "clusters", according to the degree of overlap between them. Each cluster was then given a unique identifying index, the molecular cluster index (MCI).

An MCI identifies a set of matched features on different images. Thus an MCI represents a protein or proteins eluting at equivalent positions in the 2D separation in different samples.

6.1.12. Construction of Profiles

After matching all component gels in the study to the final composite master image, the intensity of each feature was measured and stored. The end result of this analysis was the generation of a digital profile which contained, for each identified feature: 1) a unique identification code relative to corresponding feature within the composite master image (MCI), 2) the x, y coordinates of the features within the gel, 3) the isoelectric point (pI) of the DFs, 4) the apparent molecular weight (MW) of the DFs, 5) the signal value, 6) the standard deviation for each of the preceding measurements, and 7) a method of linking the MCI of each feature to the master gel to which this feature was matched. By virtue of a Laboratory Information Management System (LIMS), this MCI profile was traceable to the actual stored gel from which it

was generated, so that proteins identified by computer analysis of gel profile databases could be retrieved. The LIMS also permitted the profile to be traced back to an original sample or patient.

6.1.13. Differental Analysis of the Profiles

Each MCI within the mastergroup was a potential BAD-Associated Feature (DF). The confirmation of an MCI as a definite DF was achieved by the statistical criteria specified below.

6.1.14. Statistical Analysis of the Profiles

The complementary statistical strategies specified below were used in the order in which they are listed to identify DFs from the MCIs within the mastergroup.

(a) The Wilcoxon Rank-Sum test. This test was performed between the control and the BAD samples for each MCI basis. The MCIs which recorded a p-value less than or equal to 0.05 were selected as statistically significant DFs with 95% selectivity.

(b) A second non-overlapping selection strategy is based on the fold change. A fold change representing the ratio of the average normalized protein abundances of the DFs within an MCI, was calculated for each MCI between each set of controls and BAD samples. An 80% confidence limit for the mean of the fold changes was calculated. The MCIs with fold changes which fall outside the confidence limit were selected as DFs which met the criteria of the significant fold change threshold with 80% selectivity. Because the MCI fold changes are based on an 80% confidence limit, it follows that the significant fold change threshold is itself 80%.

(c) A third non-overlapping selection strategy is based on qualitative presence or absence alone. Using this procedure, a percentage feature presence was calculated across the control samples and BAD samples for each MCI which was a potential DF based on such qualitative criteria alone, i.e. presence or absence. The MCIs which recorded a percentage feature presence of 80% or more on BAD samples and a percentage feature presence of 20% or less on control samples, were selected as the qualitative differential DFs with 80% selectivity. A second group of qualitative differential DFs with 80% selectivity were formed by those MCIs which recorded a percentage feature presence of 80% or more on control samples and a percentage feature presence of 20% or less on BAD samples.

Application of these three analysis strategies allowed DFs to be selected on the basis of: (a) statistical significance as measured by the Wilcoxon Rank-Sum test, (b) a significant fold change threshold with a chosen selectivity, or (c) qualitative differences with a chosen selectivity.

6.1.15 Recovery and analysis of selected proteins

Proteins in DFs were robotically excised and processed to generate tryptic digest peptides. Tryptic peptides were analyzed by mass spectrometry using a PerSeptive Biosystems Voyager- DETM STR Matrix-Assisted Laser Desorption Ionization Time-of- Flight (MALDI-TOF) mass spectrometer, and selected tryptic peptides were analyzed by tandem mass spectrometry (MS/MS) using a Micromass Quadrupole Time-of-Flight (Q-TOF) mass spectrometer (Micromass, Altrincham, U.K.) equipped with a nanoflowTM electrospray Z-spray source. For partial amino acid sequencing and identification of DPIs, uninterpreted tandem mass spectra of tryptic peptides were searched using the SEQUEST search program (Eng et al., 1994, J. Am. Soc. Mass Spectrom. 5:976-989), version v.C.1. Criteria for database identification included: the cleavage specificity of trypsin; the detection of a suite of a, b and y ions in peptides returned from the database, and a mass increment for all Cys residues to account for carbamidomethylation. The database searched was database constructed of protein entries in the non-redundant database held by the National Centre for Biotechnology Information (NCBI) which is accessible at http://www.ncbi.nlm.nih.gov/. Following identification of proteins through spectral-spectral correlation using the SEQUEST program, masses detected in MALDI-TOF mass spectra were assigned to tryptic digest peptides within the proteins identified. In cases where no proteins could be identified through searching with raw, uninterpreted MS/MS spectra of tryptic digest peptides using the SEQUEST program, tandem mass spectra of the peptides were interpreted manually, using methods known in the art. (In the case of interpretation of low-energy fragmentation mass spectra of peptide ions see Gaskell et al., 1992, Rapid Commun. Mass Spectrom. 6:658-662)

7. EXAMPLE: DIAGNOSIS AND TREATMENT OF BAD

The following example illustrates the use of a DPI of the invention for screening or diagnosis of BAD, determining the prognosis of a BAD patient, or

monitoring the effectiveness of BAD therapy. The following example also illustrates the use of modulators (e.g., agonist or antagonists) of a DPI of the invention to treat or prevent BAD.

Dickkopf-3 (Dkk-3) belongs to a family a secreted glycoproteins that antagonise the Wnt signalling pathway. Wnts are a large family of cysteine-rich, secreted glycoproteins, which bind to frizzled seven-transmembrane-span receptors, and regulate cell fate and embryonic patterning (Eastmann and Grosschedl, Regulation of LEF-1/TCF transcription factors by Wnt and other signals, *Curr Opin Cell Biol* 1999 Apr 11:2 233-40). Recent studies suggest additional functions of Wnt regulated genes in the central nervous sytem (CNS) to promote synapse formation, an effect that can be mimicked by low dose lithium treatment (Jennings C., A signal for synapse formation, *Nature Neuroscience* 2000 Apr 3:4, 308; Hall AC, Lucas FR, Salinas PC, Axonal remodeling and synaptic differentiation in the cerebellum is regulated by WNT-7a signaling, *Cell* 2000 Mar 3 100:5 525-35). Intracellularly, Wnt signalling leads to stabilisation of cytosolic beta-catenin. In the absence of Wnts, beta-catenin is phosphorylated by glycogen synthase kinase3beta (GSK3beta), which triggers ubiquitination of beta-catenin by betaTrCP and degradation in proteasomes. Phosphorylation of beta-catenin occurs in a multiprotein complex assembled by the scaffolding protein axin or conductin.

Wnt binding to its receptor Frizzled leads to activation of the Dishevelled protein (Klingensmith J, Nusse R, Perrimon N: The Drosophila segment polarity gene dishevelled encodes a novel protein required for response to the wingless signal. *Genes Dev* 1994, 8:118-130.; Krasnow RE, Wong LL, Adler PN, Dishevelled is a component of the frizzled signaling pathway in Drosophila, Development 1995 Dec 121:12 4095-102; Theisen H, Purcell J, Bennett M, Kansagara D, Syed A, Marsh JL, Dishevelled is required during wingless signaling to establish both cell polarity and cell identity, *Development* 1994 Feb 120:2 347-60), which enhances the phosphorylation of glycogen synthase kinase (GSK) (Cook D, Fry MJ, Hughes K, Sumathipala R, Woodgett JR, Dale TC, Wingless inactivates glycogen synthase kinase-3 via an intracellular signalling pathway which involves a protein kinase C, *EMBO J* 1996 Sep 2 15:17 4526-36). GSK phosphorylation blocks its ability to phosphorylate beta-catenin, leading to increased stability and accumulation (Munemitsu S, Albert I, Rubinfeld B, Polakis P, Deletion of an amino-terminal sequence beta-catenin in vivo and promotes hyperphosporylation of the adenomatous

polyposis coli tumor suppressor protein, *Mol Cell Biol* 1996 Aug 16:8 4088-94.; Pai LM, Orsulic S, Bejsovec A, Peifer M, Negative regulation of Armadillo, a Wingless effector in Drosophila, *Development* 1997 Jun 124:11 2255-66; Yost C, Torres M, Miller JR, Huang E, Kimelman D, Moon RT, The axis-inducing activity, stability, and subcellular distribution of beta-catenin is regulated in Xenopus embryos by glycogen synthase kinase 3, *Genes Dev* 1996 Jun 15 10:12 1443-54). beta-catenin can interact with members of T cell factor (TCF)/lymphoid enhancer factor (LCF) family in the nucleus, which regulate Wnt target genes (Wodarz A, Nusse R, Mechanisms of Wnt signaling in development, *Annu Rev Cell Dev Biol* 1998 14: 59-88). Various secreted factors, such as WIF-1, cerberus (cer) and FrzB, bind to Wnts and block the interaction with frizzled proteins.

Dkk proteins are potent antagonist of Wnt signalling through an unknown mechanism. The human Dkk gene family is composed of Dkk-1, Dkk-2, Dkk-3, Dkk-4 and a unique Dkk-3 related protein termed Soggy (Sgy) (Krupnik VE, Sharp JD, Jiang C, Robison K, Chickering TW, Amaravadi L, Brown DE, Guyot D, Mays G, Leiby K, Chang B, Duong T, Goodearl AD, Gearing DP, Sokol SY, McCarthy SA, Functional and structural diversity of the human Dickkopf gene family, *Gene* 1999 Oct 1 238:2 301-13). Dkk-3 mRNA is highly expressed in brain and heart and low levels can be detected in spleen, kidney, liver, small intestine, placenta and lung (Tsuji T, Miyazaki M, Sakaguchi M, Inoue Y, Namba M, A REIC gene shows down-regulation in human immortalized cells and human tumor-derived cell lines, *Biochem Biophys Res Commun* 2000 Feb 5 268:1 20-4). Murine Dkk-3 mRNA is expressed in neurones of the cortex and hippocampus (Krupnik et al., *supra*).

In certain tumors, mutation of axin, beta-catenin or the tumor suppressor APC also lead to stabilisation of beta-catenin. beta-catenin degradation is modulated by the casein kinase CK1 and by the protein phosphatases PP2A and PP2C. Stabilised beta-catenin enters the cell nucleus and associates with TCF transcription factors, which leads to the transcription of Wnt-target genes. Smad4, Tsh, XSox17 and the histone acetyl transferase CBP modulate target gene expression. When beta-catenin is absent, certain TCFs repress transcription by interacting with the co-repressors groucho and CtBP. Phosphorylation of TCFs by a MAP-kinase pathway involving TAK1 and NLK negatively regulates Wnt signalling. beta-catenin also binds to cadherin cell adhesion molecules and provides a link to the actin cytoskeleton. Data for the Wnt pathway have been obtained from a variety of systems and organisms. The following

example illustrate the use of DPI-6, DPI-186 or DPI-192 of the invention for screening or diagnosis of a neuropsychiatric or neurological diseases, determining the prognosis of a subject having a neuropsychiatric or neurological disease, or monitoring the effectiveness of a neuropsychiatric or neurological disease therapy. The following example also illustrates the use of modulators (e.g., agonist or antagonists) of DPI-6, DPI-186, or DPI-192 of the invention to treat or prevent neuropsychiatric or neurological diseases.

A colipase fold in the carboxy-terminal domain of Dkks, in particular the second cysteine rich domain (Cys-2) may enable Dkks proteins to interact with lipids and subsequently Wnt proteins, in order to regulate Wnt function (Aravind L, Koonin EV, A colipase fold in the carboxy-terminal domain of the Wnt antagonists--the Dickkopfs, *Curr Biol* 1998 Jul 2 8:14 R477-8), since Wnt proteins are known to be tightly associated with the cell surface (Smolich BD, McMahon JA, McMahon AP, Papkoff J, Wnt family proteins are secreted and associated with the cell surface, *Mol Biol Cell* 1993 Dec 4:12 1267-75).

The expression of three isoforms, DPI-6, DPI-186 and DPI-192 of Dickkopf with molecular weights and pI values of 62182 Da and pI of 4.29, 53154 Da and pI of 4.29, 63376 Da and pI of 4.31 respectively have been shown herein to be significantly differentially expressed in the cerebrospinal fluid (CSF) of subjects having Depression as compared with the CSF of subjects free from a neuropsychiatric or neurological disease. Thus, quantitative detection of DPI-6, DPI-186 or DPI-192 in CSF can be used to diagnose neuropsychiatric or neurological diseases, determine the progression of a neuropsychiatric or neurological disease or monitor the effectiveness of a therapy for a neuropsychiatric or neurological disease.

In one embodiment of the invention, compounds that modulate (i.e., upregulate or downregulate) the expression, activity or both the expression and activity of DPI-6 are administered to a subject in need of treatment or for prophylaxis of a neuropsychiatric or neurological disease. Antibodies that modulate the expression, activity or both the expression and activity of DPI-6, DPI-186 or DPI-192 are suitable for this purpose. In addition, nucleic acids coding for all or a portion of DPI-6, DPI-186 and DPI-192, or nucleic acids complementary to all or a portion of DPI-6, DPI-186 or DPI-192, may be administered. DPI-6, DPI-186 or DPI-192, or fragments of the DPI-6, DPI-186 or DPI-192 polypeptides may also be administered.

The invention also provides screening assays to identify additional compounds that modulate the expression of DPI-6, DPI-186 or DPI-192, or activity of DPI-6, DPI-186 or DPI-192. Compounds that modulate the expression of DPI-6, DPI-186 and DPI-192 *in vitro* can be identified by comparing the expression of DPI-6, DPI-186 or DPI-192 in cells treated with a test compound to the expression of DPI-6, DPI-186 or DPI-192 in cells treated with a control compound (e.g., saline). Methods for detecting expression of DPI-6, DPI-186 or DPI-192 are known in the art and include measuring the level of DPI-6, DPI-186 or DPI-192 RNA (e.g., by northern blot analysis or RT-PCR) and measuring DPI-6, DPI-186 or DPI-192 protein (e.g., by immunoassay or western blot analysis). Compounds that modulate the activity of DPI-6, DPI-186 or DPI-192 can be identified by comparing the ability of a test compound to agonize or antagonize a function of DPI-6, DPI-186 or DPI-192 , such as its ability to block Frizzled activation, activity or the binding of Wnts to the Frizzled receptor, activation of Disheveled, GSK-3 phosphorylation, changes in expression of Wnt regulated genes, to the ability of a control compound (e.g., saline) to inhibit the same function of DPI-6, DPI-186 or DPI-192 . Compounds capable of modulating DPI-6, DPI-186 or DPI-192 binding to Wnts, or Wnts to the Frizzled receptor or DPI-6, DPI-186 or DPI-192 activity are identified as compounds suitable for further development as compounds useful for the treatment of neuropsychiatric or neurological disease.

Binding between DPI-6 and its binding partner Wnt, of the Wnt receptor Frizzled, can be determined by, for example, contacting DPI-6, DPI-186 or DPI-192 with cells known to express the Wnt and or the Frizzled receptor and assaying the extent of binding between DPI-6, DPI-186 or DPI-192 and Wnt of the cell surface receptor, or by contacting DPI-6, DPI-186 or DPI-192 with its receptor in a cell-free assay, i.e., an assay where the DPI-6, DPI-186 or DPI-192 and Wnt and or the Frizzled receptor are isolated, and, preferably, recombinantly produced, and assaying the extent of binding between DPI-6, DPI-186 or DPI-192 and Wnt and or the Frizzled receptor. Through the use of such assays, candidate compounds may be tested for their ability to agonize or antagonize the binding of DPI-6, DPI-186 or DPI-192 to its Wnt and or the Frizzled receptor.

Compounds identified *in vitro* that affect the expression or activity of DPI-6, DPI-186 or DPI-192 can be tested *in vivo* in animal models of a neuropsychiatric or

neurological disease, or in subjects having a neuropsychiatric or neurological disease, to determine their therapeutic efficacy.

The present invention is not to be limited in terms of the particular embodiments described in this application, which are intended as single illustrations of individual aspects of the invention. Functionally equivalent methods and apparatus within the scope of the invention, in addition to those enumerated herein, will be apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications and variations are intended to fall within the scope of the appended claims. The contents of each reference, patent and patent application cited in this application is hereby incorporated by reference in its entirety.

WE CLAIM:

1. An isolated nucleic acid molecule that hybridizes under highly stringent conditions or moderately stringent conditions to one or both of the following nucleic acid sequences:
GAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCCT;
GCCATCCATCTAGACCTAGAAGAATACCGG.

2. An isolated nucleic acid molecule that hybridizes under highly stringent conditions or moderately stringent conditions to the sequence listed in Figure 2A.

3. A preparation comprising an isolated peptide coded for by the nucleic acid molecule of claim 1 or claim 2.

4. A preparation comprising an isolated human protein, said protein comprising one or more of the following sequences: EWVAIESDSVQPVPR; AIHLDLEEYR.

5. The preparation according to claim 4, wherein the protein has an isoelectric point (pI) of about 4.86 and an apparent molecular weight (MW) of about 60,009.

6. The preparation according to claim 5, wherein the pI of the protein is within 10% of 4.86 and the MW is within 10% of 60,009.

7. The preparation according to claim 5, wherein the pI of the protein is within 5% of 4.86 and the MW is within 5% of 60,009.

8. The preparation according to claim 5, wherein the pI of the protein is within 1% of 4.86 and the MW is within 1% of 60,009.

FIGURE 1

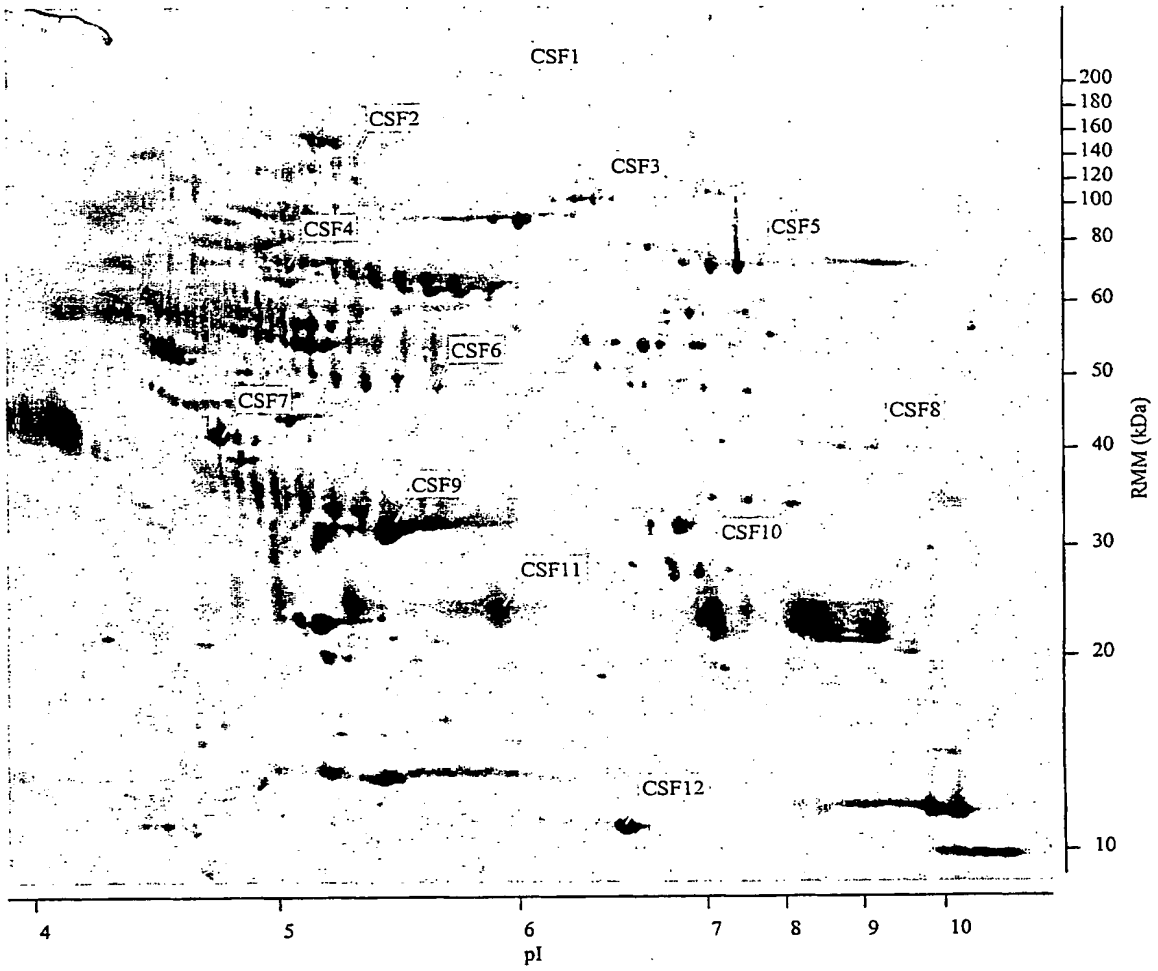

FIGURE 2

Figure 2A

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   1  gnnnnnnagn gntntannan naatgcnttt gancatggct gcgtctttgc
  51  tggctgtgct gctgctgctg ctgctggagc gcggcatgtt ctcctcaccc
 101  tccccgcccc cggcgctgtt agagaaagtc ttccagtaca ttgacctnca
 151  tcaggatgaa tttgtgcaga cgctgaagga gtgggtggcc atcgagagcg
 201  actctgtcca gcctgtgcct cgcttcagac aagagctctt canaatgatg
 251  gccgtggctg cggacacgct gcagcgcctg ggggcccgtg tggcctcggt
 301  ggacatgggt cctcagcagc tgcccgatgg tcagagtctt ccaatacctc
 351  ccgtcatcct ggccgaactg gggagcgatc ccacgaaagg caccgtgtgc
 401  ttctacggcc acttggacgt gcagcctgct gaccggggcg atgggtggct
 451  cacggacccc tatgtgctga cggaggtaga cgggaaactt tatggacgag
 501  gagcgaccga caacaaaggc cctgtcttgg cttggatcaa tgctgtgagc
 551  gccttcagag ccctggagca agatcttcct gtgaatatca aattcatcat
 601  tgaggggatg gaagaggctg gctctgttgc cctggaggaa cttgtggaaa
 651  aagaaaagga ccgattcttc tctggtgtgg actacattgt aatttcagat
 701  aacctgtgga tcagccaaag gaagccagca atcacttatg gaacccgggg
 751  gaacagctac ttcatggtgg aggtgaaatg cagagaccag gattttcact
 801  caggaacctt tggtggcatc cttcatgaac caatggctga tctggttgct
 851  cttctcggta gcctggtaga ctcgtctggt catatcctgg tccctggaat
 901  ctatgatgaa gtggttcctc ttacagaaga ggaaataaat acatacaaag
 951  ccatccatct agacctagaa gaataccgga atagcagccg ggttgagaaa
1001  tttctgttcg atactaagga ggagattcta atgcacctct ggaggtaccc
1051  atctctttct attcatggga tcgagggcgc gtttgatgag cctggaacta
1101  aaacagtcat acctggccga gttataggaa aattttcaat ccgtctagtc
1151  cctcacatga atgtgtctgc ggtggaaaaa caggtgacac gacatcttga
1201  agatgtgttc tccaaaagaa atagttccaa caagatggtt gtttccatga
1251  ctctaggact acacccgtgg attgcaaata ttgatgacac ccagtatctc
1301  gcagcaaaaa gagcgatcag aacagtgttt ggaacagaac cagatatgat
1351  ccgggatgga tccaccattc caattgccaa aatgttccag gagatcgtcc
1401  acaagagcgt ggtgctaatt ccgctgggag ctgttgatga tggagaacat
1451  tcgcagaatg agaaaatcaa caggtggaac tacatagagg gaaccaaatt
1501  atttgctgcc tttttcttag agatggccca gatccattaa tcacaagaac
1551  cttctagtct gatctgatcc actgacagat tcacctc
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Figure 2B

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1    MAASLLAVLL LLLLERGMFS SPSPPPALLE KVFQYIDLHQ DEFVQTLKEW

51   VAIESDSVQP VPRFRQELFX MMAVAADTLQ RLGARVASVD MGPQQLPDGQ

101  SLPIPPVILA ELGSDPTKGT VCFYGHLDVQ PADRGDGWLT DPYVLTEVDG

151  KLYGRGATDN KGPVLAWINA VSAFRALEQD LPVNIKFIIE GMEEAGSVAL

201  EELVEKEKDR FFSGVDYIVI SDNLWISQRK PAITYGTRGN SYFMVEVKCR

251  DQDFHSGTFG GILHEPMADL VALLGSLVDS SGHILVPGIY DEVVPLTEEE

301  INTYKAIHLD LEEYRNSSRV EKFLFDTKEE ILMHLWRYPS LSIHGIEGAF

351  DEPGTKTVIP GRVIGKFSIR LVPHMNVSAV EKQVTRHLED VFSKRNSSNK

401  MVVSMTLGLH PWIANIDDTQ YLAAKRAIRT VFGTEPDMIR DGSTIPIAKM

451  FQEIVHKSVV LIPLGAVDDG EHSQNEKINR WNYIEGTKLF AAFFLEMAQI

501  H*
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INTERNATIONAL SEARCH REPORT

Ir ational Application No
Ic./GB 01/00786

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C07K14/47 C12N15/12

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
EPO-Internal, WPI Data, PAJ, GENSEQ, EMBL, BIOSIS, CHEM ABS Data, MEDLINE, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99 58660 A (ENDRESS GREGORY A ;FLORENCE KIMBERLY (US); HUMAN GENOME SCIENCES I) 18 November 1999 (1999-11-18) abstract; claims 1-23 -& DATABASE GENSEQ 'Online! ID/AC: Y76144, 23 March 2000 (2000-03-23) "Human secreted protein encoded by gene 21." XP002168884 abstract -& DATABASE GENSEQ 'Online! ID/AC: Z65270, 23 March 2000 (2000-03-23) "Human secreted protein gene 21" XP002168885 abstract	1-8

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[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

° Special categories of cited documents :

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"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
11 July 2001	23/07/2001

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Gundlach, B

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
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INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No
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